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Db	961	ACAGCCTTCTTACAAGGATTTTACACCTCCTTTTGGGTTGGGATCTCTGACAGTGTG	1020
Qy	1021	ATGTTGCTTAACCTATATGACAGCTGTAAACGGGCCCCGTATGTAAGTCCAAAGTCTTACGGGAA	1080
Db	1021	ATGTTGCTTAACCTATATGACAGCTGTAAACGGGCCCCGTATGTAAGTCCAAAGTCTTACGGGAA	1080
Qy	1081	TCACCGTTTGTGAACAAGCAAGAGGCGCACTGTATGCTAACGTGTCCGAAACCAAGTTAAG	1140
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Qy	1201	CTGTTGTTTACTTGTGCTGATTTCAAGAAC	1231
Db	1201	CTGTTGTTTACTTGTGCTGATTTCAAGAAC	1231
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AR381440	DEFINITION	Sequence 1 from patent US 6608038.	
AR381440	ACCESSION	AR381440	
AR381440.1	VERSION	AR381440.1	GI:40089474
KEYWORDS			
SOURCE			
ORGANISM			Unknown.
REFERENCE			Unclassified.
AUTHORS			1 (bases 1 to 1231) Caplan,S.L., Boettcher,B.R., Slosberg,E.D., Connelly,S., Kaleko,M. and Desai,U.J.
TITLE			Methods and compositions for treatment of diabetes and related conditions via gene therapy
JOURNAL			Patent: US 6608038-A 1 19-AUG-2003;
FEATURES			location/Qualifiers
source			1..1231 /organism="unknown" /mol_type="genomic DNA"
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Best Local Similarity			100.0%; Pred. No. 5e-256;
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Db	61	CCACCGCTGACCTGAAGGCCCAAGGGCTGTGAGACAGCCTCTCTCTTGGACCTCTCTCGG	120
Qy	121	CCCTAAAGGAGCTGGGCAAGCCTTCCAGACTATGTTGACTGAAGCTTCAAGCTGTG	180
Db	121	CCCTAAAGGAGCTGGGCAAGCCTTCCAGACTATGTTGACTGAAGCTTCAAGCTGTG	180
Qy	181	CCTCCACCAATGCTGTGAAGTTCTCTGGGGGAGGACACAGACGCTGTGTTTGTCAACCTC	240
Db	181	CCTCCACCAATGCTGTGAAGTTCTCTGGGGGAGGACACAGACGCTGTGTTTGTCAACCTC	240
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Db	241	GTTACTCTTCCATGTGACACAGCCAAAGGTCCGCTCTGCAATCCAGGGGGAACAACAGGCG	300
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 DEFINITION Sequence 3 from patent US 6620594.  
 ACCESSION AR39364  
 VERSION AR39364.1 GI:40141198  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1231)

AUTHORS Jacobino, J.-B., Muzzin, P. and Boss, O.  
 TITLE Unclonable protein homologue: UCP 3  
 JOURNAL Patent: US 6620594-A 3 16-SEP-2003;  
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HS084763  
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 DEFINITION Homo sapiens UCP3 mRNA, complete cds.  
 ACCESSION U84763  
 VERSION U84763.1 GI:2183020  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 (bases 1 to 1231)  
 Bosse, O., Samec, S., Paoloni-Giacchino, A., Rossier, C., Dullio, A.,  
 Seydoux, J., Muzzin, P. and Giacobino, J.P.  
 Uncoupling protein-3: a new member of the mitochondrial carrier  
 family with tissue-specific expression  
 FEBS Lett. 408 (1), 39-42 (1997)  
 JOURNAL FEBS Lett. 408 (1), 39-42 (1997)  
 MEDLINE 97324095  
 PUBMED 9180264  
 REFERENCES 2 (bases 1 to 1231)  
 Bosse, O., Samec, S., Muzzin, P., Rossier, C. and Giacobino, J.P.  
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 Submitted (11-JAN-1997) Medical Biochemistry, Faculty of Medicine,  
 University of Geneva, 1 Michel Servet, Geneva 4, GE 1211,  
 Switzerland  
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 Query Match 100.0%; Score 1231; DB 9; Length 1231;  
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 ACCESSION AX031190  
 VERSION AX031190.1 GI:10278536  
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 ORGANISM unidentified  
 REFERENCE 1  
 AUTHORS Chen, F. and Liu, Q.

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Matches 1226;	Conservative	0;	Mismatches 3;	Indels 2;
			Gaps	2

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Qy	1081	TCACCGTTTTGAACAAGACAAGAGGCCACTGGTAGCTAAGCTGTCCGAAACCAAGTTAAG	1140
Db	1271	TCACCGTTTTGAACAAGACAAGAGGCCACTGGTAGCTAAGCTGTCCGAAACCAAGTTAAG	1330
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Db	1331	AATGGAAGAAAACGGTGCATCCAGGCAACAATGAGACAGAGCCACACATGTTTACAGAA	1390
Qy	1201	CTGTTGTTTACTTGTGCTGATTCAGAAAC	1231
Db	1391	CTGTTGTTTACTTGTGCTGATTCAGAAAC	1421

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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BD106811	BD106811.1	GI:23201629					
CP	2002502240-A/11.						
	Mus musculus (house mouse)						
	Mus musculus						

REFERENCE 1 (bases 1 to 2340)  
AUTHORS Liu, Q. and Chen, F.  
TITLE Human uncoupling protein 3  
JOURNAL Patent: JP 2002502240-A 11 22-JAN-2002;  
Import: 05 FEB 2002

COMMENT	
PN	JP 2002502240-A/11
PD	22-JUN-2002
PF	19-MAY-1998 JP 1998550522
PR	20-MAY-1997 US 60/047179, 08-AUG-1997 GB 9716886.8 PR
09	-DEC-1997 US 60/069141
PI	QINGYUN LIU, FANG CHEN
PC	G07H17/00, C12P21/06, C12N1/20, C12N15/00
CC	Strandedness: Double;
CC	Topology: Linear;
PH	Key Location/Qualifiers.

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Db	193	TCCTGGATGAGAGCCCTAGGAGCCCTCTGTGCGCCCGCGTGGCAGACTCACAGCC	252	
QY	61	CCACGGCTGCACTGAAGCCCAAGGGCTGTGGACAAGCCTTCCTTGACCTCTCTGG	120	
Db	253	CCACGGCTGCACTGAAGCCCAAGGGCTGTGGACAAG-CTCTTCCTTGA-CTCTCTCTGG	310	
QY	121	CCCTAAGGACTGGGCAAGGCTTCAGAGCATATGGTGAAGCTTCAGACGTG	180	



Query Match	Similarity	93.1%;	Score 116.4;	DB 6;	Length 1193;
Best Local	Similarity	99.1%;	Pred. No.1e-237;		
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Db	46	TCCTGGATGAGACCCCTAGGAGACCCCTGTGCTGCTCCCTGCGGTGGCAGGACTCACAGCC	105		
QY	61	CCACCGCTGCATGAGAGCCCAAGGGCTGTGGAGCAGCTCTCTCTTGGACCTTCCTCGG	120		
Db	106	CCACCGCTGCATGAGAGCCCAAGGGCTGTGGAGCAGCTCTCTCTTGGACCTTCCTCGG	165		
QY	121	CCTTAAAGGAGCTGGGCAAGCCTTCCAGGACTATGTTGATGAAAGCTTTCAGAGTG	180		
Db	166	CCTTAAAGGAGCTGGGCAAGCCTTCCAGGACTATGTTGATGAAAGCTTTCAGAGTG	225		
QY	181	CCTCCACCATGAGCTGTGAAGTTCCTGGGGGCAAGCAGCAGCAGCCTGTTTGTGACCTC	240		
Db	226	CCTCCACCATGAGCTGTGAAGTTCCTGGGGGCAAGCAGCAGCAGCCTGTTTGTGACCTC	285		
QY	241	GTTACCTTTCACTGACACAGCCAAAGTTCGCTCTGCAATCCAGGGGGAGAACAGAGCG	300		
Db	286	GTTACCTTTCACTGACACAGCCAAAGTTCGCTCTGCAATCCAGGGGGAGAACAGAGCG	345		
QY	301	GTCACAGCAGCCCGGACTCGTGACAGTACCGTGGGCGTGTGGAGCACATCTGACCATGATG	360		
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QY	361	CGAGCTGAGGGTCCCTGACAGCCCTTCAATGGGCTGTGGCCCGGCTTGCACGCGCAGATG	420		
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QY	421	AGCTTGCCCTCAATCCGACATCGGCTCTATGACTCCGTCAAGCAGGTATACACCCCAAA	480		
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Db	526	GGGCGGCAACA	CTCCAGCCTCACTACCCGGATTTTGTGCGCGCTGCACCA	CAGGAGCCATG	585
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Qy	601	CTCGGGCCAT	CCAGAGCCGACAGAAAATACGGGGGCTATGACGCTTACAGAACATC		660
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Qy	721	GCTATCGTCAACTGTG	CTGAGTGTGTGACCTACGACATCTCTCAGAGAAAGCTGCTGAC		780
Db	766	GCTATCGTCAACTGTG	CTGAGTGTGTGACCTACGACATCTCTCAGAGAAAGCTGCTGAC		825
Qy	781	TACCACTGTCTCACT	GCACATTTGTCTCTGCTTTTGAGCGGCTTC		840
Db	826	TACCACTGTCTCACT	GCACATTTGTCTCTGCTTTTGAGCGGCTTC		885
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Db	886	TGTGCCCAAGTGTGTG	CTCCCGGTGAGAGTGTGTAAGACCGGGTATATGAATCACTCT		945
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Db      1066 ATGTTGTAACCTATAGAGAGCTGAAACGGGCGCTTATGAAAGTCCAGATGTTACGGGAA 1125
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Db      1126 TCACCGTTTGAACAAGACAGAGAGCCACTGTGTAGCTAAAGTGTCCGAACCAAGTTAAG 1185
Qy      1141 AATGGAAG 1148
Db      1186 AATGGAAG 1193

RESULT 10
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LOCUS      AX175157      1193 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION      Sequence 1 from Patent WO0143760.
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VERSION      AX175157.1 GI:14598561
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      1 Clapham, J.C.
TITLE      New use
PATENT      Patent: WO 0143760-A 1 21-JUN-2001;
JOURNAL      SMITHKLINE BEECHAM PLC (GB)
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Query Match      93.1%; Score 1146.4; DB 6; Length 1193;
Best Local Similarity 99.9%; Pred. No. 1e-237; Indels 0; Gaps 0;
Matches 1147; Conservative 0; Mismatches 1;

Qy      1 TCCTGGAGTGAAGCCCTGAGGAGCCCTGTGTGCTGCCCTCCGTGCGAGACTCAAGCC 60
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Qy      481 GGGGCGGCAACTCCGCTCACTACCCGATTTTGGCGGCTGCAACCAAGAGCCATG 540
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Qy      721 GCTATGTCAACTGTGCTGAGGTGTGACTTACAGACTCTCAAGAGAAAGCTGTGAG 780
Db      766 GCTATGTCAACTGTGCTGAGGTGTGACTTACAGACTCTCAAGAGAAAGCTGTGAG 825
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Qy      1081 TCACCGTTTGAACAAGACAGAGAGCCACTGTGTAGCTAAAGTGTCCGAACCAAGTTAAG 1140
Db      1126 TCACCGTTTGAACAAGACAGAGAGCCACTGTGTAGCTAAAGTGTCCGAACCAAGTTAAG 1185
Qy      1141 AATGGAAG 1148
Db      1186 AATGGAAG 1193

RESULT 11
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LOCUS      AX361226      1193 bp      DNA      linear      PAT 15-FEB-2002
DEFINITION      Sequence 1 from Patent WO0207754.
AX361226
VERSION      AX361226.1 GI:18693870
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      1 Clapham, J.C.
TITLE      New use
PATENT      Patent: WO 0207754-A 1 31-JAN-2002;
JOURNAL      SMITHKLINE BEECHAM PLC (GB)
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ORIGIN
Query Match      93.1%; Score 1146.4; DB 6; Length 1193;
Best Local Similarity 99.9%; Pred. No. 1e-237; Indels 0; Gaps 0;
Matches 1147; Conservative 0; Mismatches 1;

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QY 1 TCCTGGAGTGAAGCCCTAGAGAGCCCTGTGCTGCCCCCTGCGTGGCAGAGCTGACAGCC 60  
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 KEYWORDS JP 2002300891-A/1.  
 SOURCE unidentified  
 ORGANISM unidentified  
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 AUTHORS Beelley,L.J., Paine,K. and Godden,R.J.  
 TITLE Novel compounds  
 JOURNAL Patent: JP 2002300891-A 1 15-OCT-2002;  
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 COMMENT  
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 PN JP 2002300891-A/1  
 PD 15-OCT-2002  
 PF 08-JAN-2002 JP 2002001716  
 PR 05-MAR-1997 GB 9704551.2, 18-MAR-1997 GB 9705614.7 PR  
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 Best Local Similarity 99.9%; Pred. No. 1e-237;  
 Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TCCTGGAGTGAAGCCCTAGAGAGCCCTGTGCTGCCCCCTGCGTGGCAGAGCTGACAGCC 60  
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 AUTHORS Bealey, L. James, Paine, K. and Godden, R. James.  
 TITLES Polynucleotides and polypeptides belonging to the uncoupling proteins family

JOURNAL Patent: US 6187560-A 1 13-FEB-2001;  
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Query Match 93.0%; Score 1145.4; DB 6; Length 1192;  
 Best Local Similarity 99.9%; Pred. No. 1.7e-237;  
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QY 1 TCTGGAGATGAGAGCCCTTAGAGAGCCCTTGTGCTGCCCCCTGCGTGGCAGAGACTCAAGCC 60  
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RESULT 14
LOCUS   AF001787 1175 bp mRNA linear PRI 26-JUN-1997
DEFINITION Homo sapiens uncoupling protein 3 mRNA, complete cds.
ACCESSION AF001787
VERSION   AF001787.1 GI:2198812
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SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE 1 (bases 1 to 1175)
          Vidal-Puig,A., Solanes,G., Grujic,D., Flier,J.S. and Lowell,B.B.
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          Biochem. Biophys. Res. Commun. 235 (1), 79-82 (1997)
JOURNAL   97339440
MEDLINE   9196039
REFERENCE 2 (bases 1 to 1175)
          Vidal-Puig,A., Solanes,G., Grujic,D., Flier,J.S. and Lowell,B.B.
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     Best Local Similarity 100.0%; Pred. No. 2,1e-237;
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RESULT 15

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 ACCESSION AF011449  
 VERSION AF011449.1 GI:2440012  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1104)  
 Gong, D.-W., He, Y., Karas, M. and Reitman, M.  
 Uncoupling protein-3 is a mediator of thermogenesis regulated by  
 thyroid hormone, beta3-adrenergic agonists, and leptin  
 J. Biol. Chem. 272 (39), 24129-24132 (1997)  
 JOURNAL 97450925  
 MEDLINE 9305858  
 PUBMED 2 (bases 1 to 1104)  
 REFERENCE Gong, D.-W., He, Y., Karas, M. and Reitman, M.  
 AUTHORS Direct Submission  
 TITLE Submitted (30-JUN-1997) Diabetes Branch, NIDDK/NIH, Bldg 10/Rm  
 JOURNAL 8S235A, Bethesda, MD 20892  
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 Best Local Similarity 99.8%; Pred. No. 7.8e-228;  
 Matches 1102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
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OW nucleic - nucleic search, using SW model

Run on: May 18, 2004, 11:12:25 ; Search time 123 Seconds  
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5554.021 Million cell updates/sec

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Scoring table: IDENTITY NTC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	981.4	79.7	1132	4	US-09-808-457-3
5	981.4	79.7	1132	4	US-09-423-410-5
6	732	59.5	2782	2	US-08-937-466-1
7	732	59.5	2782	2	US-09-172-528-1
8	732	59.5	2782	3	US-09-318-199-1
9	732	59.5	2782	3	US-09-503-579-1
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14	593.8	48.2	1777	2	US-08-937-466-5
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18	476.6	38.7	1596	2	US-08-807-861A-38
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22	475.6	38.6	930	4	US-10-001-051B-1
23	457.2	37.1	1255	1	US-08-878B-38
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31	385.6	31.3	1205	3	US-09-210-681-36	Sequence 36, Appl
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## ALIGNMENTS

RESULT 1  
US-09-808-457-1  
Sequence 1, Application US/09808457

Patent No. 6608038

GENERAL INFORMATION:

APPLICANT: Boehringer, Brian

APPLICANT: Caplan, Shari

APPLICANT: Kaleko, Michael

APPLICANT: Connolly, Sheila

APPLICANT: Desai, Urvil

APPLICANT: Sloberberg, Eric

TITLE OF INVENTION: Methods and Compositions For Treatment

TITLE OF INVENTION: Of Diabetes and Related Conditions Via Gene Therapy

FILE REFERENCE: 4-31353A/USN

CURRENT APPLICATION NUMBER: US/09/808,457

CURRENT FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/XXX,XXX

PRIOR FILING DATE: 2000-03-15

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1231

TYPE: DNA

ORGANISM: Unknown

FEATURES:

OTHER INFORMATION: cDNA from clone UCP3L

US-09-808-457-1

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e-307;

Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1201 CTGTTGTTACTTGTGTGATTCAGAAAC 1231

RESULT 2  
 US-09-423-410-3  
 ; Sequence 3, Application US/09423410  
 ; Patent No. 6620594  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Giacobino, Jean-Paul

; APPLICANT: Muzzin, Patrick  
 ; APPLICANT: Bosc, Olivier  
 ; TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3  
 ; FILE REFERENCE: 4-30353/A  
 ; CURRENT APPLICATION NUMBER: US/09/423,410  
 ; CURRENT FILING DATE: 1998-11-04  
 ; EARLIER APPLICATION NUMBER: PCT/EP98/02645  
 ; EARLIER FILING DATE: 1998-05-05  
 ; EARLIER APPLICATION NUMBER: 1072/97  
 ; EARLIER FILING DATE: 1997-05-07  
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 ; SOFTWARE: PatentIn Ver. 2.0  
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 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: cDNA from clone  
 ; OTHER INFORMATION: UCP3L  
 ; US-09-423-410-3

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QY 1201 CTGTGTTTACTTGTGTCGATTCAGAAAC 1231  
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## RESULT 3

US-09-142-565-1  
; Sequence 1, Application US/09142565A  
; Patent No. 6187560  
; GENERAL INFORMATION:  
; APPLICANT: Lee James Beasley  
; APPLICANT: Kelly Paine  
; APPLICANT: Robert James  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30002  
; CURRENT APPLICATION NUMBER: US/09/142,565A  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: 9704551.2  
; EARLIER FILING DATE: 1997-03-05  
; EARLIER APPLICATION NUMBER: 9705614.7  
; EARLIER FILING DATE: 1997-03-18  
; EARLIER APPLICATION NUMBER: 97305305.1  
; EARLIER FILING DATE: 1997-07-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1192  
; TYPE: DNA  
; ORGANISM: HOMO SAPIEN  
US-09-142-565-1

Query Match 93.0%; Score 1145.4; DB 3; Length 1192;  
Best Local Similarity 99.9%; Pred. No. 2.9e-285;  
Matches 1146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTGGAGTGAAGCCCTGAGGAGCCCTGTCGTCGCTCCGTCGAGAGACTCAGAGCC 60  
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DB 61 CCAACGCTGACATGAAGCCCAAGGCTGTGAGCAGCCTCTCTCTGAGCCTCTCTCGG 120

DB 106 CCAACGCTGACATGAAGCCCAAGGCTGTGAGCAGCCTCTCTCTGAGCCTCTCTCGG 165  
QY 121 CCTTAAAGGACTGAGGAGAGCCTTCAAGACTATGTTGACTGAAGCCTTCAAGACTG 180  
DB 166 CCTTAAAGGACTGAGGAGAGCCTTCAAGACTATGTTGACTGAAGCCTTCAAGACTG 225  
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DB 226 CCTTCAACCATGCTGTGAAGTTCTGAGGAGGAGCAGACAGCCTGTTTGTGACCTTC 285  
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QY 181 CCTCCACACATGGCTGTGAAGTTCCTGGGGGAGGACAGACGCTTTTGTGACCTC 240  
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 Db 421 AGCTTCGCTCCATCCGATCGAGCTCTATGATCCGCTCAAGAGGTGTACACCCCAAA 480  
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 Db 541 GGGGTGACCTGTGCGCCAGGCCACAGATGTGTGAAGTCCGATTTTCAAGGCCATACAC 600  
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 Db 601 CTCGGGCGATCCAGAGGACAGAAATACAGCGGAGCTATGAGCCCTACAGAACATC 660  
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 QY 961 ACAGCTTCTACAAAGGATTTTACACCTCTCT 991  
 Db 961 ACAGCTTCTACAAAGGATTTTACACCTCTCTCT 991

## RESULT 6

US-08-937-466-1

Sequence 1, Application US/08937466

Patent No. 5846779

GENERAL INFORMATION:

APPLICANT: Zhang, Ning

APPLICANT: Amaral, M. Catherine

APPLICANT: Chen, Jin-long

TITLE OF INVENTION: UCP3 Genes

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE &amp; TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/937,466  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-009  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2782 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-937-466-1

Query Match 59.5%; Score 732; DB 2; Length 2782;  
 Best Local Similarity 81.1%; Pred. No. 9e-179;  
 Matches 904; Conservative 0; Mismatches 195; Indels 15; Gaps 4;  
 QY 4 TGGGATGAGACCTTGAAGGAGCCCTGTGTGCTGCCCTGCGCGTGGAGACTCAAGCCCA 63  
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 QY 64 CCGCTGCACTGAAGCCAGGAGCTGTGAGCAAGCTTCTCTTGAACCTTCTGAGCC 123  
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 Db 681 GG---AAGTGAAGAGAGAGAAATACAGAGGAGCTATGATGCTTACAGAACATGCGC 737

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OY	724	ATCGTCAACTGTGTGAGTGTGACCTACGACATCTCTCAAGAGAAAGCTGTGACTAC	783
Db	798	ATTGTCAACTGTGTGAGATGTGACCTACGACATCATCAAGAGAAAGTTCTGTGAAGCT	857
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Db	858	CACCTGTTACTGACAACTTCCCTGTGACTTTGTCTGTGCTTTGGAGCTTCGTCTGT	917
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Db	918	GCACAGTGTGTGCTCTCCCGGTGATGTGTGAAGACCCGATCATGAACGCTCCCTCA	977
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Db	978	GGCCAGTACTCCGACGCCCTCTGTGACTGTATGTGTGAAGATGTGTGGCCCTCAAGAGAGGCCCA	1037
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Db	1038	GCCTTCTTCAAGAGGATTTGTGTGCTCTCTTTCTGTGCGTCTGTGAAGCTGATATGATG	1097
OY	1024	TTTCGTAACTTATGACAGCTGAAGACGGGCGCTGATGAAAGTCCAGATGTTACGGGAATCA	1083
Db	1098	TTTGTAACTATATGACCACTGAAGAGGGCGCTTAATGAAGATGCCAGGTACTGCGGGGAATCT	1157
OY	1084	CGCTTTGAACAAGACAAGAGGCCACTGTGAC	1117
Db	1158	CGGTTTGAACAAGCAAGACAGGCGCTGCTGAATC	1191

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[illegible]

QY 964 GCCTTCACAGGATTTACACCTCTTTTGGGATTCCTGGAACGTGGTATG 1023  
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QY 1024 TTGGAACCTATGACAGCTGAAAGGCGCCGTATGAAAGTGCAGATGTTACGGGAATCA 1083  
DB 1098 TTGGAACCTATGACAGCTGAAAGGCGCCGTATGAAAGTGCAGATGTTACGGGAATCT 1157  
QY 1084 CCGTTTGAACAAGACAGAGGCGCACTGGTAGC 1117  
DB 1158 CCGTTTGAACAAGACAGAGGCGCTGCGTAAC 1191

## RESULT 8

US-09-318-199-1  
Sequence 1, Application US/09318199  
Patent No. 6025469

## GENERAL INFORMATION:

APPLICANT: Zhang, Ning  
APPLICANT: Amaral, M. Catherine  
APPLICANT: Chen, Jin-Long  
TITLE OF INVENTION: UCP3 Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/318,199

## FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/937,466

## ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2782 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-318-199-1

## Query Match

Best Local Similarity 59.5%; Score 732; DB 3; Length 2782;  
Pred. No. 9e-179; Indels 15; Gaps 4;  
Matches 904; Conservative 0; Mismatches 195;

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QY 64 CCGCTGCACTGAAGCCCAAGAGCCCTGTGAGAGAGCCCTCTCTCTGGAAGCTCTTGGAGCC 123  
DB 152 TCCTTAACCTGAAGCAAGAGATTCAGAGAGCCCTCTCTCTGGAAGCTCTTGGAGAGCAGC 211  
QY 124 TAAAGGAGCTGGGAGAGCCCTTCAGAGAGTATGATGAGTGAAGGCTTCAGAGCTGAGCCT 183

DB 212 AAAGAACAGAGCCATTCC--CCGAGACATGATGAGACTTCAAGCCCTCCGAAGTGCT 269  
QY 184 CCCACAGAGCTGAGAGATTCCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243  
DB 270 CCCACAGAGCTGAGAGATTCCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329  
QY 244 ACCCTTCACTGAGACAG 303  
DB 330 ACTTTTCCCTGAG 389  
QY 304 CAG 363  
DB 390 CAGA-----GAGTCAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440  
QY 364 ACTGAGAGTCCCTGAG 423  
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QY 424 TTGAGCTCATTCGAG 483  
DB 501 TTGAGCTCATTCGAG 560  
QY 484 GCGACAACTCCAG 543  
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QY 544 GTGACCTGTGAG 603  
DB 621 GTGACCTGTGAG 680  
QY 604 GGGGCAATCCAG 663  
DB 681 GG--AACTGAG 737  
QY 664 AGGAG 723  
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QY 724 ATGCTCACTGTGAG 783  
DB 798 ATGCTCACTGTGAG 857  
QY 784 GACCTGCTCACTGAG 843  
DB 858 GACCTGCTCACTGAG 917  
QY 844 GCGACAG 903  
DB 918 GCGACAG 977  
QY 904 GCGCAGTACTTGAAG 963  
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QY 1024 TTGTAACCTATGAG 1083  
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QY 1084 CCGTTTGAACAAGACAGAGGCGCACTGGTAGC 1117  
DB 1158 CCGTTTGAACAAGACAGAGGCGCTGCGTAAC 1191

## RESULT 9

US-09-503-579-1

Sequence 1, Application US/09503579  
Patent No. 6248561  
GENERAL INFORMATION:  
APPLICANT: Zhang, Ning













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STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-172-528-5

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Query Match      48.2%; Score 593.8; DB 2; Length 1777;
Best Local Similarity 81.2%; Pred. No. 2,7e-143;
Matches 743; Conservative 0; Mismatches 157; Indels 15; Gaps 4;

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QY 124 TAAAGGACTGGGCAAGCCCTTCAGAGACTATGAGTTGAGTGAAGCTTGAAGCTTCA 183
DB 212 AAAGGAACAGGCGCAATTC-CCGGGACATGATGAGCTTCAGCCCTCGAAGTGCCT 269
QY 184 CCCACATGAGCTGTGAAGTCTCTGGGGGAGGCAAGCAGAGCTGTTTGTCTGACTGCT 243
DB 270 CCCACAGGTTGTGAAGTCTCTGGGGGAGGCAAGCTGCGGCTGTTTGTGGAGACTCTC 329
QY 244 ACCTTCCACTGAGCAGGCAAGGTCGCGCTGCAAGATCGAGGGGAGAAACAGGGGCTC 303
DB 330 ACTTTCCCTGAGCAGGCAAGGTCGCTGCAAGATCGAAGGGAGAAACAGGGGCTC 389
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DB 390 CAGA-----GCGTGAAGTACCGGCTGTGTGCTGGTACCATCTGATGATGCTGCG 440
QY 364 ACTGAGGCTGCTGAGGCGCTTCAATGAGCTGTGCGCGCTGCAAGCGCCAGATGAGC 423
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DB 561 GCGGAACTCAGAGCTCAGCTGCAATGAGATTTGCGAGCTGCAAGAGGCAATGCG 620
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DB 681 GG--AACTGAGAGAGAGAGAAAATACAGAGGGAATATGAGATGCTTACAGAACCATGCGC 737
QY 664 AGGAGAGAGAGATCAGGGGCGCTGTGTGAAAAGAACTTTGCCCAATCATAGAGATGCT 723
DB 738 AGGAGAGAGAGATCAGGGGCGCTGTGTGAAAAGGAACTTTGCCCAATCATAGAGATGCT 797
QY 724 ATGTCACTGTGTGAGGATGAGTGTGACTTGAAGATCTCTCAAGAGAGAGTGTGACTAC 783
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QY 784 CACTGTGCTGACTGACAACTTCCCTGCACTTTGTCTGTGCTTTGAGCGGCTTCTGT 843
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QY 844 GCCACAGTGTGCTTCCCGGCTGTGAGCGTGTGAAAAGCCGGATATGAACTCACTCCA 903
DB 918 GCCACAGTGTGCTTCCCGGCTGTGAGCGTGTGAAAAGCCGGATATGAACTCACTCCA 977
QY 904 GGCCAGTACTTCAAGC 918
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Job time : 129 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 13:51:52 ; Search time 588 Seconds  
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9500.575 Million cell updates/sec

Title: US-09-423-410-3

Perfect score: 1231  
Sequence: 1 tccctggatgagccctag.....ttgttcgcatcagaac 1231

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA.\*

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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	100.0	1231	9	US-09-808-457-1 Sequence 1, Appl1
2	1146.4	93.1	1193	9	US-09-826-507-1 Sequence 1, Appl1
3	1145.4	93.0	1192	9	US-09-734-134-1 Sequence 1, Appl1
4	981.4	79.7	1132	9	US-09-808-457-3 Sequence 3, Appl1
5	981.4	79.7	1132	10	US-09-823-868-5 Sequence 5, Appl1
6	490	39.8	1575	9	US-09-917-800A-1679 Sequence 1679, Ap
7	490	39.8	1575	12	US-10-152-319A-1731 Sequence 1731, Ap
8	476.6	38.7	1505	10	US-09-823-868A-3 Sequence 131, Ap
9	476.6	38.7	1505	10	US-09-823-868A-3 Sequence 3, Appl1
10	476.6	38.7	1612	15	US-10-240-965-183 Sequence 183, App
11	476.6	38.7	1643	15	US-10-240-965-183 Sequence 183, App
12	476.6	38.7	1646	16	US-10-159-563-344 Sequence 344, App
13	475.6	38.6	930	9	US-09-884-814-7 Sequence 7, Appl1
14	475.6	38.6	930	14	US-10-001-051B-1 Sequence 1, Appl1

15	475.6	38.6	930	16	US-10-197-019-2 Sequence 2, Appl1
16	474	38.5	930	9	US-09-884-814-2 Sequence 2, Appl1
17	474	38.5	930	9	US-09-884-814-5 Sequence 5, Appl1
18	474	38.5	930	15	US-10-265-689-2 Sequence 2, Appl1
19	451.6	36.7	960	10	US-09-567-856-1 Sequence 1, Appl1
20	442.2	35.9	1187	13	US-10-336-472-129 Sequence 129, App
21	441.8	35.9	847	9	US-09-734-134-5 Sequence 5, Appl1
22	326.8	26.5	924	10	US-09-823-868A-1 Sequence 1, Appl1
23	326.8	26.5	924	17	US-10-641-643-890 Sequence 890, App
24	274.4	22.3	416	9	US-09-960-352-387 Sequence 3287, App
25	254.4	20.7	512	9	US-09-736-457-1014 Sequence 1014, App
26	254.4	20.7	512	9	US-09-902-941-1014 Sequence 1014, App
27	254.4	20.7	512	9	US-09-849-628-1014 Sequence 1014, App
28	254.4	20.7	512	13	US-10-283-017-1014 Sequence 1014, App
29	254.4	20.7	512	15	US-10-017-754-1014 Sequence 1014, App
30	254.4	20.7	512	15	US-10-113-872-1014 Sequence 1014, App
31	245.2	19.9	674	17	US-10-404-460-263 Sequence 263, App
32	227.8	18.5	573	17	US-10-332-859-107 Sequence 107, App
33	223	18.1	567	13	US-10-332-859-107 Sequence 9562, App
34	223	18.1	967	16	US-10-027-632-9562 Sequence 9562, App
35	213.8	17.4	1021	16	US-10-321-039-59 Sequence 59, Appl1
36	201	16.3	222	9	US-09-734-134-3 Sequence 3, Appl1
37	196.2	15.9	816	13	US-10-037-417-25 Sequence 25, Appl1
38	194.2	15.8	1331	13	US-10-425-114-27120 Sequence 27120, A
39	184.6	15.0	764	9	US-09-910-943-628 Sequence 628, App
40	162	13.2	318	9	US-09-736-457-1376 Sequence 1376, App
41	162	13.2	318	9	US-09-902-941-1376 Sequence 1376, App
42	162	13.2	318	9	US-09-849-628-1376 Sequence 1376, App
43	162	13.2	318	13	US-10-283-017-1376 Sequence 1376, App
44	162	13.2	318	15	US-10-017-754-1376 Sequence 1376, App
45	162	13.2	318	15	US-10-113-872-1376 Sequence 1376, App

## ALIGNMENTS

RESULT 1  
US-09-808-457-1  
X Sequence 1, Application US/09808457 056608038

Patent No. US20020065239A1  
GENERAL INFORMATION:  
APPLICANT: Boettcher, Brian  
APPLICANT: Caplan, Shari  
APPLICANT: Kaleko, Michael  
APPLICANT: Connolly, Shella  
APPLICANT: Desai, Urv  
APPLICANT: Slosberg, Eric  
TITLE OF INVENTION: Methods and Compositions For Treatment of Diabetes and Related Conditions Via Gene Therapy  
FILE REFERENCE: 4-31353A/USN  
CURRENT APPLICATION NUMBER: US/09/808,457  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/XXX,XXX  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1231  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: cDNA from clone UCP3L  
US-09-808-457-1

Query Match 100.0%, Score 1231, DB 9, Length 1231;  
Best Local Similarity 100.0%, Pred. No. 0;  
Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGGATGAGACCCCTAGGAGACCCCTGTCGCGCCCTGCGACAGACTCACAGCC 60  
DB 1 TCCTGGATGAGACCCCTAGGAGACCCCTGTCGCGCCCTGCGACAGACTCACAGCC 60  
QY 61 CCACCGCTGCATGAGCCAGGCGTGTGAGAGACGCTCTCTCTTGTGACCTCTCTCGG 120

[illegible]

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Qy	1201	CTGTTGTTTACTTGTGCTGATTTGAAGAAC	1231
Db	1201	CTGTTGTTTACTTGTGCTGATTCAGAAAC	1231

RESULT 2  
US-09-826-507-1  
; Sequence 1, Application US/09826507  
; Patent No. US20020004492A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee James Beesley  
; APPLICANT: John Christopher Clapham  
; APPLICANT: Robert James Godden  
; TITLE OF INVENTION: NEW USE  
; FILE REFERENCE: GH-3009-C1  
; CURRENT APPLICATION NUMBER: US/09/826,507  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/312,620  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 9814926.3  
; PRIOR FILING DATE: 1998-07-09  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1193  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-826-507-1

Query Match	93.1%;	Score 1146.4;	DB 9;	Length 1193;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1147;	Conservative	0;	Mismatches	1;
			Indels	0;
			Gaps	0;

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Qy	61	CCACGCGTGCAGTGAAGCCCAAGGCGTGTGAGAGAGCCCTCTCTCTTGGACCTCTCTGGG	120
Db	106	CCACGCGTGCAGTGAAGCCCAAGGCGTGTGAGAGAGCCCTCTCTCTTGGACCTCTCTGGG	165
Qy	121	CCCTAAAGGAGCTGGGCGAGAGCCTTCCAGAGCTATGTTTGGACTGAACCTTCAGACCTG	180
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Qy	181	CCTCCACCAATGCGCTGTGAAGTTCTCGGGGGCAGGCAAGAGCGCTGTTTGTGACCTC	240
Db	226	CCTCCACCAATGCGCTGTGAAGTTCTCGGGGGCAGGCAAGAGCGCTGTTTGTGACCTC	285
Qy	241	GTTACCTTTCACATGAGACACAGCCAGGTCGCGCTTCAGATTCAGAGGGGAGAACAGAGCG	300
Db	286	GTTACCTTTCACATGAGACACAGCCAGGTCGCGCTTCAGATTCAGAGGGGAGAACAGAGCG	345
Qy	301	GTCAGAGCGGCCGCGCTGTGCGAGTACCGTGGCGTGTGCTGGGCAACAATCTTGAACATGTGG	360
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Qy	361	CGGACTGAGGGTCCCTGAGAGCCCTTACAAATGGGCGTGTGGCCGCGCTGCAGGCGCAGATG	420
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Qy	421	AGCTTCGCGCTCATCGAGTCGCGCTCTATGACTCCGTCAGACAGGTGTACACCCCAAA	480
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Qy	541	GCGGTGACCTGTGCCAGGCCCAACAATGTGTGAGAGTCCGATTTCAAGCGCAGCATTAAC	600





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 Oy 1141 AATGGA 1147  
 Db 1186 AATGGA 1192

# RESULT 4

US-09-808-457-3  
 ; Sequence 3, Application US/09808457  
 ; Patent No. US20020065239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boettcher, Brian  
 ; APPLICANT: Caplan, Shari  
 ; APPLICANT: Kaleko, Michael  
 ; APPLICANT: Connelly, Sheila  
 ; APPLICANT: Desai, Urv  
 ; APPLICANT: Slosberg, Eric  
 ; TITLE OF INVENTION: Methods and Compositions For Treatment  
 ; TITLE OF INVENTION: of Diabetes and Related Conditions Via Gene Therapy  
 ; FILE REFERENCE: 4-31353A/USN  
 ; CURRENT APPLICATION NUMBER: US/09/808,457  
 ; PRIOR FILING DATE: 2001-03-14  
 ; PRIOR APPLICATION NUMBER: 60/XXX,XXX  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1132  
 ; TYPE: DNA  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: cDNA from clone UCP3s  
 ; US-09-808-457-3

Query Match 79.7%; Score 981.4; DB 9; Length 1132;  
 Best Local Similarity 99.4%; Pred. No. 1.1e-277;  
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
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 Oy 541 GCGGTGACTGTGCTGAGAGCCCAAGATGTGTGAAGTTCGATTTGAGGCGAGATAC 600  
 Db 541 GCGGTGACTGTGCTGAGAGCCCAAGATGTGTGAAGTTCGATTTGAGGCGAGATAC 600  
 Oy 601 CTGGGCGCATCAGAGGAGCAAGAAATACAGCGGAGCTATGAGAGCTTACAGAACATC 660  
 Db 601 CTGGGCGCATCAGAGGAGCAAGAAATACAGCGGAGCTATGAGAGCTTACAGAACATC 660  
 Oy 661 GCCAGAGAGAGAGTCAAGGAGCTGTGAGAAAGAACTTTGCCCAATCATAGAGAT 720  
 Db 661 GCCAGAGAGAGAGTCAAGGAGCTGTGAGAAAGAACTTTGCCCAATCATAGAGAT 720  
 Oy 721 GCTATCTGAACTGTGCTGAGAGTGTGACTTACGACATCTTCAAGAGAACTGTGAC 780  
 Db 721 GCTATCTGAACTGTGCTGAGAGTGTGACTTACGACATCTTCAAGAGAACTGTGAC 780  
 Oy 781 TACCACTGCTCAGTGAACAATTGCCCGCACTTTGCTGCTTGGAGCGGCTTC 840  
 Db 781 TACCACTGCTCAGTGAACAATTGCCCGCACTTTGCTGCTTGGAGCGGCTTC 840  
 Oy 841 TGTGCAAGAGTGTGCTCCCGGTGAGCGTGTGAGAACCCGGTATATGAACTCACT 900  
 Db 841 TGTGCAAGAGTGTGCTCCCGGTGAGCGTGTGAGAACCCGGTATATGAACTCACT 900  
 Oy 901 CCAGGCGAGTACTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 960  
 Db 901 CCAGGCGAGTACTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 960  
 Oy 961 ACAAGCTTCTCAAGGAGTTTACACCCCTCT 991  
 Db 961 ACAAGCTTCTCAAGGAGTTTACACCCCTCT 991

## RESULT 5

US-09-823-886A-5  
 ; Sequence 5, Application US/09823886A  
 ; Publication No. US20030150022A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Newell, Martha  
 ; APPLICANT: Berry-Lowe, Sandra  
 ; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants  
 ; FILE REFERENCE: C1102/7002  
 ; CURRENT APPLICATION NUMBER: US/09/823,886A  
 ; CURRENT FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: US 60/193,533  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1132  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-823-886A-5

Query Match 79.7%; Score 981.4; DB 10; Length 1132;  
 Best Local Similarity 99.4%; Pred. No. 1.1e-277;  
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Oy 1 TCCTGGATGAGACCTTAGAGAGCCCTGTGCTGCCCTGCGGTGAGACTCAAGCC 60  
 Db 1 TCCTGGATGAGACCTTAGAGAGCCCTGTGCTGCCCTGCGGTGAGACTCAAGCC 60  
 Oy 61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCTTGAACCTCTCTCG 120  
 Db 61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCTTGAACCTCTCTCG 120

QY 121 CCTTAAAGGAGTGGGAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 180  
 DB 121 CCTTAAAGGAGTGGGAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 180  
 QY 181 CCTTAAAGGAGTGGGAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 240  
 DB 181 CCTTAAAGGAGTGGGAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 240  
 QY 241 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 300  
 DB 241 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 300  
 QY 301 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 360  
 DB 301 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 360  
 QY 361 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 420  
 DB 361 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 420  
 QY 421 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 480  
 DB 421 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 480  
 QY 481 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 540  
 DB 481 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 540  
 QY 541 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 600  
 DB 541 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 600  
 QY 601 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 660  
 DB 601 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 660  
 QY 661 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 720  
 DB 661 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 720  
 QY 721 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 780  
 DB 721 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 780  
 QY 781 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 840  
 DB 781 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 840  
 QY 841 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 900  
 DB 841 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 900  
 QY 901 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 960  
 DB 901 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 960  
 QY 961 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 1020  
 DB 961 GTTACCTTTCAGTGAAGAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 1020

## RESULT 6

US-09-917-800A-1679  
 Sequence 1679, Application US/09917800A  
 Patent No. US20020119462A1  
 GENERAL INFORMATION:  
 APPLICANT: Mendick, Donna  
 APPLICANT: Porter, Mark  
 APPLICANT: Johnson, Kory  
 APPLICANT: Castle, Arthur  
 APPLICANT: Elashoff, Michael  
 APPLICANT: Gene Logic, Inc.  
 TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5038-US  
 CURRENT APPLICATION NUMBER: US/09/917,800A  
 PRIOR FILING DATE: 2001-07-31  
 PRIOR APPLICATION NUMBER: US 60/222,040  
 PRIOR FILING DATE: 2000-07-31  
 PRIOR APPLICATION NUMBER: US 60/222,880  
 PRIOR FILING DATE: 2000-11-02  
 PRIOR APPLICATION NUMBER: US 60/290,029  
 PRIOR FILING DATE: 2001-05-11  
 PRIOR APPLICATION NUMBER: US 60/290,645  
 PRIOR FILING DATE: 2001-05-15  
 PRIOR APPLICATION NUMBER: US 60/292,336  
 PRIOR FILING DATE: 2001-05-22  
 PRIOR APPLICATION NUMBER: US 60/295,798  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: US 60/297,457  
 PRIOR FILING DATE: 2001-06-13  
 PRIOR APPLICATION NUMBER: US 60/298,884  
 PRIOR FILING DATE: 2001-06-19  
 PRIOR APPLICATION NUMBER: US 60/303,459  
 PRIOR FILING DATE: 2001-07-09  
 NUMBER OF SEQ ID NOS: 1740  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 1679  
 LENGTH: 1575  
 TYPE: DNA  
 ORGANISM: Rattus norvegicus  
 FEATURE:  
 OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM\_019354  
 US-09-917-800A-1679

Query Match 39.8%; Score 490; DB 9; Length 1575;  
 Best Local Similarity 71.3%; Pred. No. 2.6e-133;  
 Matches 694; Conservative 0; Mismatches 265; Indels 15; Gaps 3;

QY 147 CAGGACTATGTTGAGTGAAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 206  
 DB 147 CAGGACTATGTTGAGTGAAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 206  
 QY 338 CAGGACTATGTTGAGTGAAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 397  
 DB 338 CAGGACTATGTTGAGTGAAGGCTTCCAGACTATGTTGACTGAAGCTTCAAGCGT 397  
 QY 207 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 266  
 DB 207 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 266  
 QY 398 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 457  
 DB 398 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 457  
 QY 267 GGTGCGGCTGAGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323  
 DB 267 GGTGCGGCTGAGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323  
 QY 458 AGTCCGCTGAGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 517  
 DB 458 AGTCCGCTGAGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 517  
 QY 324 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383  
 DB 324 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383  
 QY 518 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 577  
 DB 518 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 577  
 QY 384 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443  
 DB 384 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443  
 QY 578 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 637  
 DB 578 GTACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 637  
 QY 444 CCTTATGACTCCGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 503  
 DB 444 CCTTATGACTCCGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 503  
 QY 638 CCTTATGACTCCGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 694  
 DB 638 CCTTATGACTCCGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 694  
 QY 504 TACCGGAGTTTGGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 563  
 DB 504 TACCGGAGTTTGGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 563  
 QY 695 GAGCGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 754  
 DB 695 GAGCGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 754  
 QY 755 AGATGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 805  
 DB 755 AGATGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 805  
 QY 624 AAAATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 683  
 DB 624 AAAATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 683  
 QY 806 GAGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 865  
 DB 806 GAGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 865  
 QY 684 CCTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 743  
 DB 684 CCTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 743

Db 866 CCTGTGAAAAGGACCTCTCCCAATGTTGCCGAAATGCCATTGCACTGTAAGCT 925  
 Qy 744 GGTGACCTACGACATCTCTCAGAGAGAGCTGTGATACCACTGCTCACTGACAACTT 803  
 Db 926 GGTGACCTATGACCTATCAAGATATCTCTGAAAGCAACCTATGACAGAGACT 985  
 Qy 804 CCCCTGCACTTGTCTCTGCTTTGAGACCGCTTCTGTGACAGAGTGTGCTCCCTCC 863  
 Db 986 CCTTGTCCACTTCACTTCTGCTTGGGGGCGCTTGTGACACCGTATGCTCTCCCTCC 1045  
 Qy 864 GGTGACGTGTGAGAGACCGGATATGAACTCACTCCAGGCGAGTATTCAGCCCTT 923  
 Db 1046 CTTGATGTGTGTCAGACAGATATATGAACTCTGCTTGGGCGAGTACACAGCGCG 1105  
 Qy 924 CCACTGTATGATTAAGATGTGGCCCGAGAGAGGCGCCACAGCTTCTCAAGAGATTTAC 983  
 Db 1106 CCACTGTGCTCTGACCATCTCCGAGAGAGAGGCGCCGAGACCTTCTCAAGAGGCTTCA 1165  
 Qy 984 ACCCTCTTTTGTGCTTGGGATCTGTGAACTGTGTGATGTTCTGTAACCTATGAGAGCT 1043  
 Db 1166 GCTTCTCTTCTCTGCTTGGGATCTGTGAACTGTGTGATGTTCTGTAACCTATGAGAGCT 1225  
 Qy 1044 GAAAGGCGGCTGTGATGAAGTCCAGATGTTAAGGAGATGACCGTTTGAACAAGACAGA 1103  
 Db 1226 CAAAGGCGGCTGTGATGCTGCTATGATCCGAGAGGACCTTTGAGCTCTTCAGC 1285  
 Qy 1104 AGGCCACTGTAGC 1117  
 Db 1286 TGATGACTGTAGC 1299

# RESULT 7 US-10-152-319A-1731

Sequence 1731, Application US/10152319A

Publication No. US20040072160A1

## GENERAL INFORMATION:

APPLICANT: Mendrick, Donna

APPLICANT: Porter, Mark

APPLICANT: Johnson, Kory

APPLICANT: Hise, Brandon

APPLICANT: Castle, Arthur

APPLICANT: Elshof, Michael

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5089-US

CURRENT APPLICATION NUMBER: US/10152,319A

CURRENT FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: US 60/292,335

PRIOR FILING DATE: 2001-05-22

PRIOR APPLICATION NUMBER: US 60/297,523

PRIOR FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/298,925

PRIOR FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US 60/303,810

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,807

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,808

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/315,047

PRIOR FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: US 60/324,928

PRIOR FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/330,867

PRIOR FILING DATE: 2001-11-01

PRIOR APPLICATION NUMBER: US 60/330,462

PRIOR FILING DATE: 2001-10-22

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2221

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 1731

LENGTH: 1575

TYPE: DNA

ORGANISM: Rattus norvegicus

; FEATURE:  
 ; OTHER INFORMATION: Genbank Accession No. NM\_019354  
 ; US-10-152-319A-1731

Query Match 39.8%; Score 490; DB 12; Length 1575;  
 Best Local Similarity 71.3%; Pred. No. 2,6e-133;  
 Matches 694; Conservative 0; Mismatches 265; Indels 15; Gaps 3;

Qy 147 CAGACATATGTTGAGTGAAGCTTCAAGAGTGTCTCCACATAGCTGTGAATGTTCT 206  
 Db 338 CAGATATATGTTGTTTCAAGGCGACAGATGTGCCCCACAGACCGTGTAAATGTTCT 397  
 Qy 207 GGGGGCAGGACAGAGAGCTGTTTGTGACCTCGTTACCTTTCACACTGGAACAGCCAA 266  
 Db 398 GGGGGCTGGAGAGAGAGCTGTTTGTGACCTCGTTACCTTTCACACTGGAACAGCCAA 457  
 Qy 267 GGTCCGCTGACATCCAGGAGGAGAACAGAGCG--GTCCAGACGCGCGGCTGTGCA 323  
 Db 458 AGTCCGCTGACATCCAGGAGGAGATCAAGGCTAAGGCGCACCGCGCGAGCGCCCA 517  
 Qy 324 GTACGCTGCTGTGCTGGGCAACATCTGACATGCTGTGCGGACTGAGGGTCTCTGACGCC 383  
 Db 518 GTACGCGCGGCTGTGCTGGGCAACATCTGACATGCTGTGCGGACTGAGGGTCTCTGACGCC 577  
 Qy 384 CTACATATGCTGTGTGCTGGGCTGACGCGGCTGACGATGAGCTTCCGCTCATCGGATGG 443  
 Db 578 CTACATATGCTGTGTGCTGGGCTGACGCGGCTGACGATGAGCTTCCGCTCATCGGATGG 637  
 Qy 444 CCTATGATCTCGTCAAGCAGTGTACACCCCAAGGCGGAGCAATCCAGGCTTCAC 503  
 Db 638 CCTTACAGCTCTGTAAAGAGTTTCTACA---CAAGGCTCAAGGCAATGAGGATGG 694  
 Qy 504 TACCGGATTTTGGCGGCTGACCAAGAGACCATGCGGTGACTGTGCTCCAGCCAC 563  
 Db 695 GAGCGGCTCTGTGAGGATGACCAAGATGCTGCTGTGCTGTGCTGTGCTGTGCTGTG 754  
 Qy 564 AGATGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623  
 Db 755 AGATGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 805  
 Qy 624 AAAATACAGCGGAGCTATGAGCGCTTACAGAACATCGCCAGAGAGAGAGAGTCAAGG 683  
 Db 806 GAGATACAGAGACATGTGAGAGCTTACAGAACATGTGACAGAGAGAGAGTCCGGGG 865  
 Qy 684 CCTGTGAAAGAGACTTGTCCCAATCATATGAGAAATGCTATGCTCAATGCTGTAGGT 743  
 Db 866 CCTGTGAAAGAGACTTGTCCCAATCATATGAGAAATGCTATGCTCAATGCTGTAGGT 925  
 Qy 744 GGTGACCTACGACATCTCTCAGAGAGAGTGTGACCTCACTGACCTGACCAACTT 803  
 Db 926 GGTGACCTATGACCTCTATCAAGATATCTCTGAAAGCAACCTATGACAGACCT 985  
 Qy 804 CCCCTGCACTTGTCTCTGCTTTGAGACCGCTTCTGTGACAGTGTGCTCTCCCTCC 863  
 Db 986 CCTTGTCCACTTCACTTCTGCTTGGGGGCGCTTGTGACACCGTATGCTCTCCCTCC 1045  
 Qy 864 GGTGACGTGTGAGAGACCGGATATGAACTCTCACTCCAGGCGAGTATTCAGCCCTT 923  
 Db 1046 CTTGATGTGTGTCAGACAGATATATGAACTCTGCTTGGGCGAGTATCAACAGCGCGG 1105  
 Qy 924 CCACTGTATGATTAAGATGTGGCCCGAGAGAGGCGCCACAGCTTCTCAAGAGATTTAC 983  
 Db 1106 CCACTGTGCTCTGACCATCTCCGAGAGAGAGGCGCCGAGACCTTCTCAAGAGGCTTCA 1165  
 Qy 984 ACCCTCTTTTGTGCTTGGGATCTGTGAACTGTGTGATGTTCTGTAACCTATGAGAGCT 1043  
 Db 1166 GCTTCTCTTCTCTGCTTGGGATCTGTGAACTGTGTGATGTTCTGTAACCTATGAGAGCT 1225  
 Qy 1044 GAAAGGCGGCTGTGATGAAGTCCAGATGTTAAGGAGATACCGTTTGAACAAGACAGA 1103  
 Db 1226 CAAAGGCGGCTGTGATGCTGCTATGATCCGAGAGGACCTTTGAGCTCTTCAGC 1285  
 Qy 1104 AGGCCACTGTAGC 1117



DB 836 GCCCTCTTCCGCTGGGTTCTCGAGAGTGTGATGTCACCTATGACAGCT 895  
 QY 1044 GAAAGGCGCCCTGATGAAAGTCAATGTATGAGGAATCACCGTTTGAAC 1094  
 DB 896 GAAAGAGCCCTCATGCTGCTGCACTTCCGAGAGGCTCCCTTCTAGC 946

## RESULT 9

US-09-823-886A-3  
 ; Sequence 3, Application US/09823886A  
 ; Publication No. US20030150022A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Newell, Martha  
 ; APPLICANT: Berry-Lowe, Sandra  
 ; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants  
 ; FILE REFERENCE: C1102/7002  
 ; CURRENT APPLICATION NUMBER: US/09/823,886A  
 ; CURRENT FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: US 60/193,533  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: Patent version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1105  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-823-886A-3

Query Match 38.7%; Score 476.6; DB 10; Length 1105;  
 Best Local Similarity 71.2%; Pred. No. 2e-129;  
 Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3;

QY 147 CAGGACTATGTTGACTGAAGCTTCAAGCTGCTCCCAATGAGCTGTGAATTCCT 206  
 DB 82 CAGCATCATGTTGGTTGAGGTTCAAGGCCAAGATGTCCTTACCTGCACTGTGAAGTTCT 141  
 QY 207 GGGGGGAGGACAGCAGCGCTGTTTGTCTGACCTGTTACCTTTCACCTGAGACAGCCAA 266  
 DB 142 TGGGGCTGGACAGCTGCTGCTGATCGCAATCTCACTTCTCTGTGATGCTTAA 201  
 QY 267 GGTCCGCTGCAAGATCAGAGGGGAGAACAG--CGGTTCAGACGCGCGCTGTGCA 323  
 DB 202 AGTCCGCTTACAGATCAGAGAGAAAGTACGGGGCCAGTGGCGGTCAAGCCAGCCCA 261  
 QY 324 GTACCTGCGTGTGCGGACCATCTTACCATGATGTCGAGACTGAGAGGTCCTGCAAGCC 383  
 DB 262 GTACCCGCGTGTGATGCGGACCATCTGACATGATGTCGAGAGGCGCCCGAAGCCT 321  
 QY 384 CTACATATGCGTGTGCGCGCGCTGAGCGGCGAGATGAGCTTGCCTCCATCCGATCGG 443  
 DB 322 CTACATATGCGTGTGCGCGCGCTGAGCGGCGCAATGAGCTTGTCTGTCCGATCGG 381  
 QY 444 CCTCTATGACTCCGTCAAGAGGTGTACACCCCAAGAGCGAGACAATCCAGCTTCA 503  
 DB 382 CCTGTATGATCTGTGAAGATTCTACA---CAAAGGCTGTGAGATCCAGCAATGG 438  
 QY 504 TACCGGATTTGGCGGCTGCAACCAAGAGCAATGGCGGTGACCTGTGCCCCAGCCAC 563  
 DB 439 GAGCCGCTCTGAGAGGAGCAACAGAGTGCCTGCGTGTGCTGTGCGCCAGCCAC 498  
 QY 564 AGATGTGTGCAAGTCCGATTTTCAAGGCGAGCATACCTGAGGCAATCCAGAGCAAG 623  
 DB 499 GATGTGTGTAAGTCCGATTTCAAGC-----TCAAGCCCGAGCTGAGAGTGTG 549  
 QY 624 AAATACAGCGGACTATGAGCGCTTACAGAACCATCCAGAGGAGAGAGTCAAGGG 683  
 DB 550 GATATCCAAAGCAGCTCAATGCTTACAGAGCATTCGCCAGAGAGAGGTTCCGAGG 609  
 QY 684 CTTGTGAAAGAACTTTGCCCAATCATGAGGAATGTCTATGCTCACTGTCTAGAT 743  
 DB 610 CCTCTGAAAGAGGACCTCTCCCAATGTGTGCTGTAAATGCAATGTCTCACTGTGAGCT 669

QY 744 GATGACTTACAGATCTCTCAAGAGAGAGCTGCTGACTTCACTGTCTCACTGACACTT 803  
 DB 670 GATGACTTATGACCTTCAATCAAGATGCGCTCTGAAGCCAACTCATGACATGAGACT 729  
 QY 804 CCCCTGCACTTTTCTCTGCTTTGAGCGCGGCTTGTGCAAGTGTGAGTGTGCTCC 863  
 DB 730 CCTTGCACCTTCACTTGTGCTTTGGGAGAGGCTTCTGCACTGATGATGCTCC 789  
 QY 864 GATGACGTGTGAGAGCCCGATATATGATCACTTCCAGGCGATATCTTCAAGCCCT 923  
 DB 790 TGTAGACGTGTCAAGAGATATCATGATCACTTCCCTGAGGCGATAGAGGCTGG 849  
 QY 924 GACTGTATATTAAGATGTGCGCCAGAGAGGCGCCCAAGCTTCTTCAAGAGATTAC 983  
 DB 850 CCAGTGTCCCTTACATGCTTCCAGAGAGAGGCGCCGAGGCTTCTTCAAGAGGTTAT 909  
 QY 984 ACCCTCTTTTGGTGGATCCGTGAGAGTGTGATGTTGTAATCTATGACAGCT 1043  
 DB 910 GCCCTCTTCTCCGCTTGGGTTCTGGAAGTGTGATGTTCTGACCTATGAGCAGCT 969  
 QY 1044 GAAAGGCGCCCTGATGAAAGTCCAGATGTTCAGGAAATCACCGTTTGAAC 1094  
 DB 970 GAAAGAGCCCTCATGCTGCTGCTGCACTTCCGAGAGGCTCCCTTCTAGC 1020

## RESULT 10

US-10-265-689-13  
 ; Sequence 13, Application US/10265689  
 ; Publication No. US2003011975A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SURMIT, RICHARD S.  
 ; APPLICANT: COLBINS, SHEILA A.  
 ; APPLICANT: WARDEN, CRAIG H.  
 ; APPLICANT: SELDIN, MICHAEL F.  
 ; APPLICANT: RICQUIER, DANIEL  
 ; APPLICANT: BOUTLAND, FREDERIC  
 ; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN  
 ; FILE REFERENCE: 1579-376  
 ; CURRENT APPLICATION NUMBER: US/10/265,689  
 ; CURRENT FILING DATE: 2002-10-08  
 ; PRIOR APPLICATION NUMBER: US/09/353,645  
 ; PRIOR FILING DATE: 1999-07-15  
 ; PRIOR APPLICATION NUMBER: PCT/US97/06864  
 ; PRIOR FILING DATE: 1997-04-22  
 ; PRIOR APPLICATION NUMBER: 60/034,960  
 ; PRIOR FILING DATE: 1997-01-15  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: Patent Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 1612  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-265-689-13

Query Match 38.7%; Score 476.6; DB 15; Length 1612;  
 Best Local Similarity 71.2%; Pred. No. 2.3e-129;  
 Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3;

QY 147 CAGGACTATGTTGACTGAAGCTTCAAGAGGCTCCACATGAGCTGTGAAGTTCT 206  
 DB 338 CAGCATCATGTTGGTTGAGGTTCAAGGCCAAGATGTCCTTACCTGCACTGTGAAGTTCT 397  
 QY 207 GGGGGGAGGACAGCAGCGCTGTTTGTCTGACCTGTTTCACTTTCACCTGAGACAGCCAA 266  
 DB 398 TGGGGCTGGACAGCTGCTGATGCAATGCAATCTTCTCTGGAATCTCTTAA 457  
 QY 267 GGTCCGCTGCAAGATCAGAGGGGAGAACAG--CGGTTCAGACGCGCGCGCTGTGCA 323  
 DB 458 AGTCCGCTTACAGATCAGAGGAGAAAGTCAAGGGCCAGTGGCGGTCAAGCCAGCCCA 517  
 QY 324 GTACCTGCGTGTGCGGACCATCTTCAAGATGATGTCGAGAGGTCCTGCAAGCC 383  
 DB 518 GTACCCGCGTGTGATGAGGACCATTTCTTACATGATGTCGATCTGAGAGGCGCCGAAAGCCT 577



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QY 384 CTACATGAGGCTGTGGCCGCGCTGCAAGGCGCAGATGAGCTTCCGCTTCATCCGATCGG 443
DB 578 CTACATGAGGCTGTGGCCGCGCTGCAAGGCGCAGATGAGCTTCCGCTTCATCCGATCGG 637
QY 444 CCTTATGACTCCGTCAGAGAGTGTACACCCCAAGGCGCGGAGACACTCCAGCTCAC 503
DB 638 CCTTATGACTCCGTCAGAGAGTGTACACCCCAAGGCGCTGAGACAGCAGCAGATTCGG 694
QY 504 TACCGGAGTTTGGCCGCGCTGCAAGGCGCAGATGAGCTTCCGCTTCATCCGATCGG 563
DB 695 GAGCGGCTCTTACAGAGGAGAGCAGAGAGTCCCTGCTGTGCTGTGGCCCAAGCCAC 754
QY 564 AGATGTGTGAAGTCCGATTCAGGCGCAGATACCTCGGCGCATTCAGAGAGCAGAG 623
DB 755 GATGTGTGAAGTCCGATTCAGGCGCAGATACCTCGGCGCATTCAGAGAGCAGAG 805
QY 624 AAAATACAGCGGAGCTATGAGAGCCTTACAGAACATTCGCGAGAGAGAGAGTCAAGG 683
DB 806 GAGATACAGAGAGCAGTCAATGCTTACAGAGAGCAGATTCGCGAGAGAGAGTTCG 865
QY 684 CCGTGGAGAGAGAGCTTGGCCCAATCATGAGAGAGTGTATGCTATGCTATGCTGAGGT 743
DB 866 CCGTGGAGAGAGAGCTTGGCCCAATCATGAGAGAGTGTATGCTATGCTATGCTGAGGT 925
QY 744 GGTGACCTTACGACATCTCTCAAGAGAGAGTGTCTGAGCTTACACCTGCTCACTGACAACTT 803
DB 926 GGTGACCTTACGACATCTCTCAAGAGAGAGTGTCTGAGCTTACACCTGCTCACTGACAACTT 985
QY 804 CCGCTGCGCATTTGTCTGCTCTTGGAGCCGCTTCTGTGCGACAGTGTGGCTTCCG 863
DB 986 CCGCTGCGCATTTGTCTGCTCTTGGAGCCGCTTCTGTGCGACAGTGTGGCTTCCG 1045
QY 864 GGTGAGCGAGTGAAGAGCCGAGTATGAGACTCATCCAGAGCAGTATCTTCAAGCCCT 923
DB 1046 TGTAGCGTGTGTACAGAGAGATGATGATCTTGTGCTGAGAGAGTGTAGAGAGCT 1105
QY 924 CGACTGTATGATTAAGAGTGTGCGCCAGAGAGGCGCCCAAGAGCTTGTACAGAGAGT 983
DB 1106 CCGCTGTGCGCTTACATGCTCTCAAGAGAGAGGCGCCCAAGAGCTTGTACAGAGAGT 1165
QY 984 ACCCTCTTTTGGCTTGGAGTCTTGGAGAGCGTGTGATGTTGTGTAACCTATAGAGAGCT 1043
DB 1166 GCGCTCTTTTGGCTTGGAGTCTTGGAGAGCGTGTGATGTTGTGTAACCTATAGAGAGCT 1225
QY 1044 GAAACGGGCGCTGATGAAGTCCAGATGTTACGAGATCAACGCTTTTGAAC 1094
DB 1226 GAAACGGGCGCTGATGAAGTCCAGATGTTACGAGATCAACGCTTTTGAAC 1276

```

## RESULT 11

US-10-240-965-183

Sequence 183, Application US/10240965

Publication No. US20030165924A1

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: SHIFFMAN, DOV

APPLICANT: SOMOGYI, Roland

APPLICANT: LAWN, Richard M.

APPLICANT: SEITZNER, Jeffrey J.

APPLICANT: PORTER, Gordon J.

APPLICANT: MIKITA, Thomas

APPLICANT: TAI, Julie

APPLICANT: TAI, Julie

TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION

FILE REFERENCE: PA-0025 PCT

CURRENT APPLICATION NUMBER: US/10/240, 965

PRIOR FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: 60/195,106

NUMBER OF SEQ ID NOS: 276

SOFTWARE: PERL Program

SEQ ID NO 183

LENGTH: 1643

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 093687.6.
US-10-240-965-183

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Query Match 38.7%; Score 476.6; DB 15; Length 1643;
Best Local Similarity 71.2%; Pred. No. 2,3e-129;
Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3;

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QY 147 CAGGACTATGTTGAGTGAAGCTTCAAGAGTGCCTCCACATGAGCTGTGAAGTCT 206
DB 366 CAGGACTATGTTGAGTGAAGCTTCAAGAGTGCCTCCACATGAGCTGTGAAGTCT 425
QY 207 GGGGCGAGGAGAGAGCTTGTGTGCTGACCTCTGTACCTTTTCACTGTGACAGCCAA 266
DB 426 TGGGCTGAGAGAGCTGCTGTGATGAGATTTCACTCTTCTGTGATGCTTAA 485
QY 267 GGTGCGCTGAGATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
DB 486 AGTCCGCTTACAGATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
QY 324 GTACCGTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
DB 546 GTACCGTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
QY 384 CTACATGAGGCTGTGGCCGCGCTGCAAGGCGCAGATGAGCTTCCGCTTCATCCGATCGG 443
DB 606 CTACATGAGGCTGTGGCCGCGCTGCAAGGCGCAGATGAGCTTCCGCTTCATCCGATCGG 665
QY 444 CCTTATGACTCCGTCAGAGAGTGTACACCCCAAGGCGCGGAGACACTCCAGCTCAC 503
DB 666 CCTTATGACTCCGTCAGAGAGTGTACACCCCAAGGCGCTGAGCAGTGTGAGAGAGAG 722
QY 504 TACCGGAGTTTGGCCGCGCTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563
DB 723 GAGCGGCTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 782
QY 564 AGATGTGTGAAGTCCGATTCAGGCGCAGATACCTCGGCGCATTCAGAGAGAGAGAG 623
DB 783 GATGTGTGAAGTCCGATTCAGGCGCAGATACCTCGGCGCATTCAGAGAGAGAGAG 843
QY 624 AAAATACAGCGGAGCTATGAGAGCTTACAGAACATTCGCGAGAGAGAGAGAGAGAG 683
DB 844 GAGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY 684 CCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
DB 894 CCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
QY 744 GGTGACCTTACGACATCTCTCAAGAGAGAGTGTCTGAGCTTACACCTGCTCACTGACAACTT 803
DB 954 GGTGACCTTACGACATCTCTCAAGAGAGAGTGTCTGAGCTTACACCTGCTCACTGACAACTT 1013
QY 804 CCGCTGCGCATTTGTCTGCTCTTGGAGCCGCTTCTGTGCGACAGTGTGGCTTCCG 863
DB 1014 CCGCTGCGCATTTGTCTGCTCTTGGAGCCGCTTCTGTGCGACAGTGTGGCTTCCG 1073
QY 864 GGTGAGCGTGTGAAGAGCCGAGTATGAGACTCATCCAGGCGAGTATCTTCAAGCCCT 923
DB 1074 TGTAGCGTGTGTACAGAGAGATGATGATCTTGTGCTGAGAGAGTGTAGAGAGCT 1133
QY 924 CGACTGTATGATTAAGAGTGTGCGCCAGAGAGGCGCCCAAGAGCTTGTACAGAGAGT 983
DB 1134 CCGCTGTGCGCTTACATGCTCTCAAGAGAGAGGCGCCCAAGAGCTTGTACAGAGAGT 1193
QY 984 ACCCTCTTTTGGCTTGGAGTCTTGGAGAGCGTGTGATGTTGTGTAACCTATAGAGAGCT 1043
DB 1194 GCGCTCTTTTGGCTTGGAGTCTTGGAGAGCGTGTGATGTTGTGTAACCTATAGAGAGCT 1253
QY 1044 GAAACGGGCGCTGATGAAGTCCAGATGTTACGAGATCAACGCTTTTGAAC 1094

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Oy	451	GAATCCGCTCAAGAGAGGTGTACACCCCCAAAGAGGCGGGAACAATCCAGGCTCACTACCCGG	510
Ds	301	GAATTCGTCAACAGTTTCTACA---CCAGGGCTCTAGACATGCGACGATTTGGGAGCCCG	357
Oy	511	ATTTTGGCCGGCTGCACCAACAGAGCCATGGCGGTGACCTGTGCTCCAGGCCCAAGATGTG	570
Ds	358	CTCTAGACGACACACCAACAGGTGCCCTGGCTGTGGCTGTGGCCACGACCCAGATGTG	417
Oy	571	GTTAAAGTCCGATTTTCAGGCGCAGATACACTCGGGGCGATCAGAGGCGACAGAAATAC	630
Ds	418	GTTAAAGTCCGATTTCCAAAGC-----TGAGGCCGGGCTGGAGTGTGTGGAGATAC	468
Oy	631	AGCGGACATAATGACGCGCTACAGAACCATCGCCAGGAGGAAAGATCAGGGGCTGTGG	690
Ds	469	CAAGGACCCGTCAATGCTGTACAAGACATTTGCCGAGAGGAAAGGTTCCGGGGCTCTGG	528
Oy	691	AAAGGAACTTTGGCCCAACATCATAGGAAATCTATCTGCAACTGTGCTGAGGTGTGAC	750
Ds	529	AAAGGGACCTCTCCCAATGTGTCTGTATGCCATTTGCAACTGTGTGACACTGTGATACC	588
Oy	751	TAGACATCCCTCAAGGGAAGCTGTGTGACATACACCGCTCACTGACAACTTCCCGTCG	810
Ds	589	TATACCTTCATCAAGGATGCCCTCTGTAAAGCAACTCATGACAGATGAACTTCCCTTGC	648
Oy	811	CACTTTGTCTCTGCTTTTGGAGCCGGCTCTGTGCAACGTGTAGCCCTCCCGGTGAC	870
Ds	649	CACTTCAATTTCTGCTTTGGGGCAGGGCTTGTGACCACTGTCAATGCTCCCTCTGTAGAC	708
Oy	871	GTTGTGAAGACCCGGTATATGATCACTCACTCAGAGCCAGTACTTCAAGCCCCCTGTGACT	930
Ds	709	GTTGTCAAGACGAATATCATGAACTCTGCCCCGTGGCCAGTACAGTAAAGGCTGGCCACTGT	768
Oy	931	ATGATTAAGATGTGTGGCCACAGAGGGCCCCACAGCCTTCTCAAGAGGATTTTAAACCTTCC	990
Ds	769	GCCCTTACATGCTTCAGAAAGAGGGGCCCGAGCCTTCTCAAGAGGTTTATGCTCTCC	828
Oy	991	TTTTTGGCTTTGGGATCTCTGGAACGTGTGTATGTTCTGTAACCTTATGACACCTGAACCG	1050
Ds	829	TTTCTCGGCTTGGGATCTCTGGAACGTGTGTATGTTCTGCACTTATGACACGTAACGA	888
Oy	1051	GCCCTGATGAAGTTCAGATGTTACGGGAATCACCGTTTGA	1092
Ds	889	GCCCTCATGGCTGCTGTGCACTTCCCGAAGGCTCCCTTCTTA	930

## RESULT 14

US-10-001-051B-1  
Sequence 1, Application US/10001051B  
Publication No. US20020172958A1  
GENERAL INFORMATION:  
APPLICANT: Gonzalez-Zulueta, Mirella  
APPLICANT: Shamloo, Mehrdad  
APPLICANT: McFarland, K.C.  
APPLICANT: Chin, Daniel  
APPLICANT: Mieloch, Tadeusz  
APPLICANT: Melcher, Thorsten  
APPLICANT: Act Therapeutics, Inc.  
TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING  
TITLE OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES  
FILE REFERENCE: 019488-003010US  
CURRENT APPLICATION NUMBER: US/10/001,051B  
CURRENT FILING DATE: 2002-06-25  
PRIORITY APPLICATION NUMBER: US 60/244,946  
PRIORITY FILING DATE: 2000-11-01  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 930  
TYPE: DNA  
ORGANISM: Unknown Organism  
FEATURES:  
OTHER INFORMATION: Description of Unknown Organism: Any animal

OTHER INFORMATION: source, typically mammalian, most typically human  
US-10-001-051B-1

Query Match	38.6%;	Score 475.6;	DB 14;	Length 930;
Best Local Similarity	71.4%;	Pred. No. 3.8e-129;		
Matches 673;	Conservative 0;	Mismatches 254;	Indels 15;	Gaps 3;

QY	154	ATGGTGTGACCTGAAAGCCTTGCAGACCTGCGCTCCACCAATGGCTGTGAAGTTCTCGGGGGCA	213
Db	1	ATGGTGTGGTTCAAGGGCCACAGATGTGCCCCCTTACCTGCACTGTGAAGTTCTTGGGGCT	60
QY	214	GGCACACAGACCTGTATTGCTGACCTCGTTACCTTTCCATTGACACAGCCCAAGTCCGC	273
Db	61	GGCACACTGCTGCTGCATCGCAGATCTATACACTTTTCTCTGGATACTGGCTAAAGTCCGG	120
QY	274	CTGCAGATCCAGGGGGGAACCAAG---CGGTCCAGACGGCCGGCTTCGTGCACTACCGT	330
Db	121	TTACAGATCCCAAGGAGAAAGTCAAGGGGCGCAGGTGGCGCTTCACGCCAGCGCCCACTACCGC	180
QY	331	GGCGTGCCTGGGCACACATCTGACCAATGATGTCGGACTGAGGGGTCCCTGACGCCCTACAT	390
Db	181	GGTGTGATGGGCACCAATTTGCACCATGATGTGTGATCTAGAGGGCCCCCGAAGCTTTACAT	240
QY	391	GGCGCTGAGCGCGGCTGCAAGCGCCAGATGAGTTCGCTTCATCCGCTATCGGCTCTAT	450
Db	241	GGCGCTGTGTCGGGCTCGACGGCCCAATAGCTTTTGCTGTGTCGGATGTGGCTGTAT	300
QY	451	GACTCCGTCAGACGAGTGTACACCCCAAAAGCGCGGACAACTCCAGCTCTACACCCGG	510
Db	301	GATTCGTGCAAAAGTTCTTACA---CCAAAGGCTCTAGACATGCAACATTTGGAGCGCGC	357
QY	511	ATTTTGGCCGGCTGCACACAGAGAGCATGGCGGTGACCTGTGCGCCAGGCCACAGATGTG	570
Db	358	CTCTAGAGGACACACACAGGTGCGCTGTGTGTGCTGTGGCCACGCCACAGATGTG	417
QY	571	GTGAAGGTCGATTTCAAGCGCAGCATACCTCGGGCATTCACAGACGACAGAAAATAC	630
Db	418	GTAAAGTCCGATTTCCAAGC-----TCAGGCCGGGGTGGAGGTGGTGGAGATAC	468
QY	631	AGCGGACATATGACGCGCTTACAGAACATATGCCACAGGAGAGAGATCAGGGGCTGTGG	690
Db	469	CAAAGCACCGTCMAATGCTTACAAACCACTTGCCGAGAGGAAAGGGTTCCGGGGCTCTGGG	528
QY	691	AAAGGAACCTTGGCCCAACATCATAGAGAAATGTATGCTACATGTGCTGAGGTGTGACC	750
Db	529	AAAGGACCTCTCCCAATGTGTCTGTATATGCCATTGTCAACTGTGTGAGCTGTGACC	588
QY	751	TACGACATCTCTCAGAGAGAAAGCTCTGTGACTACACACTGTCTCACTGCACAACTTCCCTGC	810
Db	589	TATGATCTCATCAAGATAGCCCTCTGTAAAGCCAACTCATGACAGATGACTCTCCCTTG	648
QY	811	CACTTTGTCTGTGCGCTTTGAGCGCGGCTTCTGTGCAACATGTGTGGCTCTCCCGGTGAC	870
Db	649	CACTTTCATTTCTGCTTTGGGGCAGGCTTCTGCAACCACTGTCAATCGCTCTCCCTGTAGAC	708
QY	871	GTGTGGAAGACCCGGTATATATGATCTCACTCAAGCCAGTACTTCAGCGCCCTGTGACTGT	930
Db	709	GTGTGCAAGAGATATATATATATATATATCTGTGCGCTGTGGCCAGTACATGAGGCTGTGCCACTGT	768
QY	931	ATGATTAAGATGTGTGGCCACAGAGGGGCCCAAGCGCTTCTACAGAGGATTTTACACCTTCC	990
Db	769	GCCCTTACATGCTTCCAGAAAGAGGGGGCCCGAGCTTCTTACAAAGGTTTATGCCCCCTC	828
QY	991	TTTTTGGCTTTGGATCTCTGGAACGTGTGTATGTTCTTAACCTTATAGACACTTAACCG	1056
Db	829	TTTCTCCGCTTGGGTTCTGTGAAAGTGTGTATGTTCTGTCACCTTATGACACTGAACGA	888
QY	1051	GCCCTGATGAAGTCCAGATGTATAGGGAATCACCGTTTGA	1092
Db	889	GCCCTCATGTGCTGTGCATTTCCCGAAGGCTCTCCCTTCTTA	930

## RESULT 15

US-10-197-019-2  
 ; Sequence 2, Application US/10197019  
 ; Publication No. US20030207284A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chew, Anne  
 ; APPLICANT: Denton, R. Rex  
 ; APPLICANT: Gilson, Christopher Raleigh  
 ; APPLICANT: Nandabalan, Krishnan  
 ; APPLICANT: Parks, Katie E.  
 ; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE  
 ; FILE REFERENCE: MMH-0042US  
 ; CURRENT FILING DATE: 2002-07-16  
 ; PRIOR APPLICATION NUMBER: US/10/197,019  
 ; PRIOR FILING DATE: 2001-01-25  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 930  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-197-019-2

Query Match 38.6%; Score 475.6; DB 16; Length 930;  
 Best Local Similarity 71.4%; Pred. No. 3.8e-129;  
 Matches 673; Conservative 0; Mismatches 254; Indels 15; Gaps 3;

OY 154 ATGGTTGACGTAAGCCCTTCAAGAGTGCCTCCACCATGGCTGTAAGTTCCTGGGGCA 213  
 DB 1 ATGGTTGAGTTCAAGGCCCAAGATGTGCCCTTACTGCCACTGTAAAGTTCTTGGAGCT 60  
 OY 214 GGCACAGCAGCCTGTTTGTCTGACCTCGTTACCTTTCCACTGACACAGCCAGGTCCGC 273  
 DB 61 GGCACAGCTGCTGATGAGATCTCATCACTTTCTGTGATGATCTTAAGTCCGG 120  
 OY 274 CTGCAATCCAGGGGGAACCAAG--CGGTCCAGAGGCCCGGCTGTGTACCTGT 330  
 DB 121 TTACAGATCCAAAGGAAGTCAAGGGCCAGTGCCTGCTACAGCCAGCCAGTACCGC 180  
 OY 331 GGCCTGCTGGGACATCCTGACCAATGGTGGGAGTCCCTGACGCCCTTACAT 390  
 DB 181 GGTGTGATGGGACCATTTGACATGTGGCTGATGAGGCCCTCCGAAAGCTTACAT 240  
 OY 391 GGGCTGTGTGCGCGCTGACAGCCAGATGAGCTTGCTCCATCCGATCGGCTCTAT 450  
 DB 241 GGGCTGTGTGCGCGCTGACAGCCCAATGAGCTTTGCTGTGCGATGGCTGTAT 300  
 OY 451 GACTCGTCAAGCAGGTGTACACCCCAAGGCGGAGACATCCAGCTCACTACCGG 510  
 DB 301 GATTCGTCAACAGTTCTTACA---CMAAGGCTCTGAGCATGCCAGATTGGAGCCGC 357  
 OY 511 ATTTGGCCGGCTGACACAGAGCATGGCGGTGACCTGTGCCAGGCCACAGATGT 570  
 DB 358 CTCTTAGAGGAGACACACAGGTGCCCTGTGGCTGTGGCCCAAGCCACGATGTG 417  
 OY 571 GTGAAGTCCGATTTCAAGGCCAGCATACCTCGGGCCATCCAGAGCCACAGAAATAC 630  
 DB 418 GTAAAGTCCGATTTCAAGC-----TCAAGCCCGGCTGAGGTGTGCGAGATAC 468  
 OY 631 AGCGGACTATGAGAGGCTTACGAACCATCGCCAGGAGAGAGATCAAGGGCCCTGTGG 690  
 DB 469 CAAGCACCCTCAATGCTTACAGACCATTCGCCGAGAGAGGTTCCGGGGCCCTGTGG 528  
 OY 691 AAAGGAATTTGCCCAACATCATAGGAATGCTATGCTCACTGTGCTGAGGTGTGACC 750  
 DB 529 AAAGGAATTTGCCCAATGCTGTGCTGTATGCTATGCTATGCTGTGCTGTGCTGTGACC 588  
 OY 751 TACGACATCTCAAGAGAGAGCTGTGACTACACCTGTGCTCACTGACAACTTCCCTTGC 810  
 DB 589 TATGACCTCATAGAGATGCCCTCTGGAAGCCACCTCATGACAGATGACCTCCCTTGC 648  
 OY 811 CACTTGTCTGCTTGTGAGCGGCTTGTGTGACCAAGTGTGGCTTCCCGGTGAGAC 870

DB 649 CACTTCATTTCTGCTTTGGGGCAGGCTTGTGACACACTGTGATGCTCCCTGTAGAC 708  
 OY 871 GTGTGAAGACCCGCTATATGAACTCACTCCAGGCCAGTACTTCAAGCCCTGACTGT 930  
 DB 709 GTGTCAAGACGAGATACATGAATCTGCTCCCTGGGCCAGTACAGTAGCGCTGGCCACTGT 768  
 OY 931 ATGATTAAGATGTGCGCCCAAGAGGCCCAAGCCTTCTCAAGAGGATTTACACCCCTCC 990  
 DB 769 GCCCTTACAGCTCCAGAAAGAGGGGCCCGAGCCTTCTACAAAGGTTCAATGCCCTCC 828  
 OY 991 TTTTGGGTTTGGATCCTGGAAGTGTGATGTTCTGTAACCTATAGACAGCTGAAACGG 1050  
 DB 829 TTCTCGCTTGGGTTCTGTGAACGTGTGATGTTCTGACCTTATGAGCACTGAAACGA 888  
 OY 1051 GCCCTGATGAAGTCCAGATGTTACGGGAATCACCGTTTGA 1092  
 DB 889 GCCCTGATGCTGCTGCACTTCCGAGAGGCTCCCTTCTGA 930

Search completed: May 18, 2004, 16:16:22  
 Job time : 594 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 11:18:36 ; Search time 3063 Seconds  
(without alignments)  
12001.418 Million cell updates/sec

Title: US-09-423-410-3

Perfect score: 1231  
Sequence: 1 tccctggatggagccctag.....tcgttcgcatcagaagaac 1231

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapect 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_estbm:\*  
3: em\_estln:\*  
4: em\_estm:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vtl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	939	76.3	939	29	AY406944 Homo sapi
2	680.6	55.3	927	29	AY406946 Mus muscu
3	611.2	49.7	808	13	BU745943 CH2#003 H
4	595.6	48.4	602	29	AY406945 Pan trogl

5	519.2	42.2	613	9	AL596731	AL596731 DKF2p451B
6	489.4	39.8	364	11	AK054060	AK054060 Mus muscu
7	487.8	39.6	364	11	AK035298	AK035298 Mus muscu
8	486.8	39.5	930	29	AY413339	AY413339 Mus muscu
9	474	38.5	930	29	AY413337	AY413337 Homo sapi
10	448.2	36.4	1101	14	CK024683	CK024683 AGENCOURT
11	434.2	35.3	673	12	BM986146	BM986146 LM24HM001
12	432.8	35.2	612	10	BF670349	BF670349 602150226
13	423.8	34.4	1181	14	CK025514	CK025514 AGENCOURT
14	420.8	34.2	930	29	AY413338	AY413338 Pan trogl
15	405.4	32.9	927	12	BI248501	BI248501 602992916
16	394.2	32.0	938	12	BI692548	BI692548 603343091
17	388.2	31.5	404	9	AA192136	AA192136 zq02d09.x
18	385	31.3	892	12	BI904624	BI904624 603168439
19	381.6	31.0	876	14	CF374967	CF374967 AGENCOURT
20	381.2	31.0	891	14	CA474512	CA474512 AGENCOURT
21	380.8	30.9	807	12	BG757774	BG757774 602714886
22	377.6	30.7	766	12	BG976754	BG976754 602845813
23	374.6	30.4	794	12	BG968126	BG968126 602835587
24	373.6	30.3	684	14	CB446089	CB446089 697877 MA
25	369.8	30.0	739	14	CA944705	CA944705 UI-CF-FNO
26	368.4	29.9	825	14	CF147551	CF147551 AGENCOURT
27	364.6	29.6	913	14	CA787496	CA787496 AGENCOURT
28	362.4	29.4	573	12	BM986209	BM986209 LM24HM001
29	360.2	29.3	1159	14	CD501350	CD501350 CDA50-D03
30	356.8	29.0	782	10	BP974251	BP974251 602243895
31	355.4	28.9	739	14	CF766488	CF766488 CES004262
32	354.6	28.8	697	12	BG965001	BG965001 602831635
33	353.2	28.7	701	9	AI430170	AI430170 me41d08.y
34	352	28.6	909	14	CF265879	CF265879 AGENCOURT
35	351	28.5	912	14	CF266280	CF266280 AGENCOURT
36	350.8	28.5	888	14	CA474222	CA474222 AGENCOURT
37	350.4	28.5	818	12	BI904048	BI904048 603166559
38	349.6	28.4	813	14	CK017263	CK017263 AGENCOURT
39	347	28.2	850	14	CA475173	CA475173 AGENCOURT
40	345.4	28.1	739	14	CA379425	CA379425 658498 NC
41	344.2	28.0	890	13	BO960193	BO960193 AGENCOURT
42	344	27.9	832	14	CF150802	CF150802 AGENCOURT
43	342.8	27.8	742	14	CK126808	CK126808 AGENCOURT
44	342.6	27.8	764	14	CK017963	CK017963 AGENCOURT
45	340.4	27.7	932	12	BI258707	BI258707 602969874

## ALIGNMENTS

RESULT 1  
LOCUS AY406944  
DEFINITION Homo sapiens UCP3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
ACCESSION AY406944  
VERSION AY406944.1 GI:39762915  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 939)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 939)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
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ORIGIN

Query Match 76.3%; Score 939; DB 29; Length 939;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-200; Indels 0; Gaps 0;  
 Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 154 ATGGTTGAGACTGAGACCTTTCAGACGTCCTCCACCATGCTGTGAAGTTCTTGAGGAGCA 213  
 Db 1 ATGGTTGAGACTGAGACCTTTCAGACGTCCTCCACCATGCTGTGAAGTTCTTGAGGAGCA 60  
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 Oy 334 GTGCTGGGACCATCTGTCACATGCTGTCGAGTACGAGGTCCTGACGCCCTTACATAGG 393  
 Db 181 GTGCTGGGACCATCTGTCACATGCTGTCGAGTACGAGGTCCTGACGCCCTTACATAGG 240  
 Oy 394 CTGCTGGGCGGCTCTGACAGGCGCAATGAGTCTGCTCCATCCGATCGGCTCTATAGAC 453  
 Db 241 CTGCTGGGCGGCTCTGACAGGCGCAATGAGTCTGCTCCATCCGATCGGCTCTATAGAC 300  
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 Db 301 TCCGTCAGACAGTGTACACCCCAAGGCGGAGCAATCCAGCCTCACTACCCGAGT 360  
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 Oy 574 AAGGTCGCAATTCAGGCGCACTACCTCTGCGGCATCCAGAGCGACAGAAATACAGC 633  
 Db 421 AAGGTCGCAATTCAGGCGCACTACCTCTGCGGCATCCAGAGCGACAGAAATACAGC 480  
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 Oy 814 TTGTGCTGCTTGTGAGCGCGCTCTGTGACAGAGTGTGAGCTTCCCGGAGTGAAG 873  
 Db 661 TTGTGCTGCTTGTGAGCGCGCTCTGTGACAGAGTGTGAGCTTCCCGGAGTGAAG 720  
 Oy 874 GTGAAGACCCGATATATGAACTTCACTTCAAGGCACTTCAAGCCCTCGACTATAG 933  
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Oy 994 TTGGCTTTGGGATCTTGAGACGTCGTGATGTTGCTTACCTATGACGACCTGAAACGGGCC 1053  
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Oy 1054 CTGATGAAGATCCAGATGTTACGGGAATCACCGCTTTTGA 1092  
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RESULT 2  
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 LOCUS  
 DEFINITION Mus musculus UCP3 gene, VIRTUAL TRANSCRIPT, partial sequence.  
 ACCESSION AY406946  
 VERSION AY406946.1 GI:39762917  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 927)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.D., Adams,M.D. and Cargill,M.  
 Title Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 927)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.D., Adams,M.D. and Cargill,M.  
 Title Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
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Query Match 55.3%; Score 680.6; DB 29; Length 927;  
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 Matches 793; Conservative 0; Mismatches 134; Indels 12; Gaps 2;

Oy 154 ATGGTTGAGACTGAGACCTTTCAGACGTCCTCCACCATGCTGTGAAGTTCTTGAGGAGCA 213  
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 Oy 214 GGCAAGACAGCCTGTTTGTCTGACCTCTGTTACCTTTCCATGAGACACAGCCCAAGGTCGC 273  
 Db 61 GGCAAGACAGCCTGTTTGTCTGACCTCTGTTACCTTTCCATGAGACACAGCCCAAGGTCGC 120  
 Oy 274 CTGCAGATCCAGAGGGAGAACACAGCGGCTCCAGACGCGCTGATGAGTACCGTGC 333  
 Db 121 CTGCAGATCCAGAGGGAGAACACAGCGGCTCCAGACGCGCTGATGAGTACCGTGC 171  
 Oy 334 GTGCTGGGACCATCTGTCACATGCTGTCGAGTACGAGGTCCTGACGCCCTTACATAGG 393  
 Db 172 GTGCTGGGACCATCTGTCACATGCTGTCGAGTACGAGGTCCTGACGCCCTTACATAGG 231  
 Oy 394 CTGCTGGGCGGCTCTGACAGGCGCAATGAGTCTGCTCCATCCGATCGGCTCTATAGAC 453





QY 1029 AACCTATGAGCAGTGAACGGGCGCTGTGTAAGTCCAGATGTATACGGGAATCACCGTT 1088  
 DB 738 GACCTATGAGCAGTGAACGGGCGCTGTGTAAGTCCAGATGTATACGGGAATCACCGTT 797  
 QY 1089 TTGAACAAG 1097  
 DB 798 CTGAAGTAG 806  
 RESULT 4  
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 LOCUS Pan troglodytes UCP3 gene, VIRUTAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY406945  
 VERSION AY406945.1 GI:39762916  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
 REFERENCE 1 (bases 1 to 602)  
 Authors Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
 Periera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Title Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 Best Local Similarity 99.3%; Pred. No. 7e-123; Indels 0; Gaps 0;  
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 QY 491 ACTCCAGCCTACTACCGGATTTTGGCGGCGTGCACACAGAGCCATGCGTACCT 550  
 DB 1 ACTCCAGCCTACTACCGGATTTTGGCGGCGTGCACACAGAGCCATGCGTACCT 60  
 QY 551 GTGCCAGCCACAGATGTGTGTAAGTCCGATTTTGGCGGCGTGCACACATACCTCGGCGCAT 610  
 DB 61 GTGCCAGCCACAGATGTGTGTAAGTCCGATTTTGGCGGCGTGCACACATACCTCGGCGCAT 120  
 QY 611 CCAAGAGCCACAGAAATATACAGCGGAGCTATGAGACCGCTTACAGACATATGCGAGGAGG 670  
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 QY 671 AAGAGATCAGGGGCGTGTGTAAGAACTTGTGCCAATCATGAGGATGCTATGCTCA 730  
 DB 181 AAGAGATCAGGGGCGTGTGTAAGAACTTGTGCCAATCATGAGGATGCTATGCTCA 240  
 QY 731 ACTGTGTGAGTGTGTGATCAAGACATCTCAAGAGAAAGTGTGATACCACTGC 790  
 DB 241 ACTGTGTGAGTGTGTGATCAAGACATCTCAAGAGAAAGTGTGATACCACTGC 300

QY 791 TCACAGACACTTCCCTCCGACACTTGTCTGCTGTGAGACCGGCTTGTGCGACAG 850  
 DB 301 TCACAGACACTTCCCTCCGACACTTGTCTGCTGTGAGACCGGCTTGTGCGACAG 360  
 QY 851 TGTGGCCCTCCCGGTGACGCTGTGTAAGAACCCGGTATATGAACTCACCTCCAGGCCAGT 910  
 DB 361 TGTGGCCCTCCCGGTGACGCTGTGTAAGAACCCGGTATATGAACTCACCTCCAGGCCAGT 420  
 QY 911 ACTTACGCCCTCCGACACTGATATGATTAAGATGTGTGCGCCAGAGAGGCCCGACAGCTTCT 970  
 DB 421 ACTTACGCCCTCCGACACTGATATGATTAAGATGTGTGCGCCAGAGAGGCCCGACAGCTTCT 480  
 QY 971 ACAAGGATTTACACCTCTCTTTTGGCTTGGATCTGGAACGTGTGATGTTCTGTA 1030  
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 LOCUS DKFZP451B221\_r1\_451 (synonym: hlccl) spinal cord Homo sapiens cDNA  
 DEFINITION clone DKFZP451B221\_5', mRNA sequence.  
 ACCESSION AL596731  
 VERSION AL596731.1 GI:15154427  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 613)  
 Authors Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).  
 Title EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).  
 JOURNAL Unpublished (1999)  
 COMMENT Contract: MIPS  
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 Query Match 42.2%; Score 519.2; DB 9; Length 613;  
 Best Local Similarity 99.3%; Pred. No. 9.9e-106; Indels 1; Gaps 1;  
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 Best Local Similarity 99.3%; Pred. No. 9.9e-106; Indels 1; Gaps 1;  
 Matches 532; Conservative 0; Mismatches 3;

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 OY 241 GTTACCTTTCACCTGAGACAGCAAGGCTCCCTGAGAGTCAAGTCCAGGGGAGAACCAAGCGG 300  
 DB 318 GTTACCTTTCACCTGAGACAGCAAGGCTCCCTGAGAGTCAAGTCCAGGGGAGAACCAAGCGG 377  
 OY 301 GTTACCTTTCACCTGAGACAGCAAGGCTCCCTGAGAGTCAAGTCCAGGGGAGAACCAAGCGG 360  
 DB 378 GTTACCTTTCACCTGAGACAGCAAGGCTCCCTGAGAGTCAAGTCCAGGGGAGAACCAAGCGG 437  
 OY 361 CGGACTGAGAGGCTCCCTGAGAGCCCTTCAAGTGGGCTGTGAGGCGGCTGAGCGGCAAGTG 420  
 DB 438 CGGACTGAGAGGCTCCCTGAGAGCCCTTCAAGTGGGCTGTGAGGCGGCTGAGCGGCAAGTG 497  
 OY 421 AGCTTGCCTTCATTCGCTGAGAGGCTCTTATGAC-TCCGTCAAGCAAGGTATACACCCCA 479  
 DB 498 AGCTTGCCTTCATTCGCTGAGAGGCTCTTATGAC-TCCGTCAAGCAAGGTATACACCCCA 557  
 OY 480 AGGCGGAGCACTGAGAGGCTCTTATGAC-TCCGTCAAGCAAGGTATACACCCCA 535  
 DB 558 AGGCGGAGCACTGAGAGGCTCTTATGAC-TCCGTCAAGCAAGGTATACACCCCA 613

RESULT 6  
 AK054060 3641 bp mRNA linear HTC 20-SEP-2003  
 LOCUS Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN  
 DEFINITION full-length enriched library, clone:E230015118 product:uncoupling  
 protein 2, mitochondrial, full insert sequence.  
 ACCESSION AK054060  
 VERSION AK054060.1 GI:26343968  
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 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Kono, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, E., Ohara, B., Watanabe, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format

JOURNAL sequencing pipeline with 384 multicapillary sequencer  
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)  
 PUBMED 20530913  
 REFERENCE 11076861  
 AUTHORS 4  
 TITLE The RIKEN Genome Exploration Research Group Phase II Team and the  
 JOURNAL PANTOM Consortium.  
 REFERENCE Functional annotation of a full-length mouse cDNA collection  
 AUTHORS Nature 409, 685-690 (2001)  
 TITLE 5  
 JOURNAL The PANTOM Consortium and the RIKEN Genome Exploration Research  
 REFERENCE Group Phase I & II Team.  
 AUTHORS Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3641)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,  
 Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUN-2001) Yoshinide Hayashizaki, The Institute of  
 COMMENT Biomedical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,  
 URL: http://genome-gsc.riken.go.jp, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
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ORIGIN  
 Query Match 39.8%; Score 489.4; DB 11; Length 3641;

Best Local Similarity 72.0%; Pred. No. 1,1e-98;  
Matches 685; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

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Db GGGGGCAGGACAGACGCTTTTGTGACCTGTTACCTTTCCACTGACACAGCCAA 481  
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267 GGTCCGCTGACATCCAGGGGAGAGACAGGCG---GTCCAGACGGCCGGCTGTGA 323  
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444 CCTATATGCTCCGTCAGACAGCTGATCAACCCCAAGCGCGGACCACTCCAGGCTGAC 503  
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Db ACCCTCTTTTGTGCTTGGAGTCTTGGAGAGAGTGTGATCACTGCTGCTGAGGT 1249  
1130 ACCCTCTTTTGTGCTTGGAGTCTTGGAGAGAGTGTGATCACTGCTGCTGAGGT 1249  
1044 GAAAGCGGCTGATGAGAGATCAAGATGTTTACGAGATCAAGATGTTTAC 1094  
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1250 GAAAGCGGCTGATGAGAGATCAAGATGTTTACGAGATCAAGATGTTTAC 1300

RESULT 7  
AK035298 3964 bp mRNA HTc 18-sep-2003  
LOCUS AK035298  
DEFINITION Mus musculus adult male urinary bladder cDNA, RIKEN full-length  
enriched library, clone:195300110 product:uncoupling protein 2,

# ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AK035298  
AK035298.1 GI:26330581  
HTc, CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

## TITLE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20493374  
11042159

## REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Kono, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
Yamamoto, R., Watanabe, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, B., Matsumoto, K.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

## TITLE

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5 The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 3964)

## JOURNAL

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozawa, T.,  
Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsumura, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akita, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.

## TITLE

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## JOURNAL

CDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in Riken.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

## FEATURES

URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/  
 Location/Qualifiers

1.3964

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/db\_xref="MGI:2359541"

/db\_xref="taxon:10090"

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/clone\_lib="RIKEN full-length enriched mouse cDNA library"

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363..1292

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TSATGAGCTTIVASPVDVKTIRNNSALGQYHSHGHALTMKREGRATYKGFMS

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## CDS

## ORIGIN

Query Match 39.6%; Score 487.8; DB 11; Length 3964;

Best Local Similarity 71.9%; Pred. No. 2.6e-98;

Matches 684; Conservative 0; Mismatches 252; Indels 15; Gaps 3;

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 207 GGGGGCAGGACACAGAGCCTGTTTGTGCACTGCTTCACTTCACTGGAACAGCCAA 266  
 416 GGGGGCTGGAGAGCTGCTGATTCAGATTCATCTTCTGAGATACCGCCA 475  
 267 GGTCCGCTGAGATCCAGGGGAGAACCAAGCG--GTCCAGACGGCCCGCTGTGCA 323  
 476 GGTCCGCTGAGATCCAGGGGAGAACCAAGCG--GTCCAGACGGCCCGCTGTGCA 323  
 324 GTACCGTGGCTGCTGGGCAACCATCTTGAACATGTTGGGAGTGAAGGCTCCTGCA 383  
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 384 CTACAAATGGGCTGCTGGGCAACCATCTTGAACATGTTGGGAGTGAAGGCTCCTGCA 443  
 536 CTACAAATGGGCTGCTGGGCAACCATCTTGAACATGTTGGGAGTGAAGGCTCCTGCA 443  
 444 CCTATGATGCTGCTCAAGCAGTGTACACCCCAAGGCGGCAACTCCAGGCTTCA 503  
 656 CCTTCAACATCTGTCAACAGATTCTACA---CAAAGGCTCAAGAGCATGAGGATGG 712  
 504 TACCCGATTTTGGCCGCTGACCAACAGAGCCATGGGGTGAACCTGTGCCAGCCAC 563  
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 DB 1004 CCCCTGACATCTTGTCTCTGCTTGTGAGCGGCTTGTGAGCGCAAGTGGGCTCCCC 1063  
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 DB 1064 TGTGATGTGTCAAGACGATATCAATGCTCCGAGAGAGAGACCGGCTTGTGAGCGCA 1123  
 QY 924 CGACTGTATGATTAAGATGTGTGAGCGGCAAGAGCGGCAAGCTTGTCAAGAGATTAC 983  
 DB 1124 TCACTGTGCGCTTACATGCTCCGAGAGAGAGACCGGCTTGTGAGCGCAAGTATTTCA 1183  
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 QY 1044 GAAACGGGCGCTGATGAAGTCCAGATGTTACGGGAATCAAGCTTTGAACT 1094  
 DB 1244 CAAAGAGCGCTTAAGTCTGCTTACCAATCTCGGAGGACCTTTCTGAGC 1294

## RESULT 8

AY413339

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

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Db	1	ATGGTTGGTTTCAAGGCGCAAGATGTCGCCCAACAGCACTGTAAGTTCTG36969CT	60		
Qy	214	GGCAGCAGACGCTGTTTGTCTGACCTCGTGAACCTTTCCACTGGAACAAGCCAGAGTCCG	273		
Db	61	GGGACACTGCTGCATTGGCAGATCTCATCACTTTCCCTGTGATTAACGGCAAGTCCGG	120		
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Qy	331	GGCGTGCAGGACCAATCTGACACCATGAGTGGGAGCTGAGGGTCCCTGCAGCCCTTACAAT	390		
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Qy	511	ATTTTGGCGGGCTGACACCAAGAGGCATGAGCGGATGACCTGTGCGCAGGCCACAGATGTG	570		
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LOCUS	AY413337				
DEFINITION	Human sapiens UCP2 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY413337				
VERSION	AY413337.1	GI:39769299			
KEYWORDS	GS5.				
SOURCE	Human sapiens (human)				
ORGANISM	Human sapiens				

REFERENCE	AUTHORS
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
PUBMED	Mammalia; Eutheria; Primates; Carnivora; Homidae; Homo.
REFERENCE	1 (bases 1 to 930)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejelival,A.,
TITLE	Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
JOURNAL	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Snieky,J.J.,
	Adams,M.D. and Cargill,M.
	Inferring nonneutral evolution from human-chimp-mouse orthologous
	gene trices
	Science 302 (5652), 1960-1963 (2003)
	14671302
	2 (bases 1 to 930)
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejelival,A.,
	Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Snieky,J.J.,
	Adams,M.D. and Cargill,M.
	Direct Submission
	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
	Rockville, MD 20850, USA
	This sequence was made by sequencing genomic exons and ordering
	them based on alignment.
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DB	61 GGCAACAGCTGCTGTGATCGCAGATCTCACTTCTCTGTGATATCTGTAAAGTCCCG 120
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DB	121 TTACAGATCCAGGAGAAAGTCAAGGGGCGCAGTGCAGCTACAGCAGCGCCCAATACCG 180
QY	331 GCGGTGCTGGGCAACCATCTGACATGTGGGCGGCTGAGGGTCCCTGACAGCCCTTAAT 390
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QY	391 GGGCTGTGGCGGCGCTGACAGGCGCAGATGAGCTTGCCTTCATTCGATCGAGCTCTAT 450
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QY	511 ATTTTGGCGGCTGACACAGAGCCATGAGGCTGTACCTTGCCCAAGCCCAAGATGTG 570
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QY	571 GTGAAGTCCGATTTTCAGGCGCAGATACCTCGGCGCATCCAGAGCAGAGAAATAC 630
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DB	469 CAAACACCGGTCAAGTCCACAGAGCATGTGCGCAGAGAGAGGTTCCGAGGCGCTGTG 528
QY	691 AAAGAACTTTGGCCCAACATCATGAGAGATGCTATGTCATCTGTGCTGAGGTGTGACC 750



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 DEFINITION 5', mRNA sequence.  
 ACCESSION CK024683  
 VERSION CK024683.1 GI:38550607  
 KEYWORDS EST.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 1101)  
 NIH-MGC http://mgc.ncl.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgaabds-r@mail.nih.gov  
 Tissue Procurement: Len Zon, Harvard  
 cDNA Library Preparation: Open Biosystems  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLM at:  
 http://image.llnl.gov  
 Plate: LLM14821 row: 1 column: 21  
 High quality sequence stop: 915.  
 Location/Qualifiers  
 1..1101  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
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 /lab\_host="DH10B"  
 /clone\_lib="NIH\_ZGC\_10"  
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 Bulk tissue was collected from a whole adult individual  
 from the Tuebingen strain. 1st strand cDNA was primed with  
 a Not I - oligo(dT) primer, double-stranded cDNA was  
 cloned into the Not I and EcoRV sites of pEXpress-1.  
 Library was size-selected for >1 kb fragments. A

## FEATURES

source

## ORIGIN

Query Match 36.4%; Score 448.2; DB 14; Length 1101;  
 Best Local Similarity 69.4%; Pred. No. 1.1e-89;  
 Matches 641; Conservative 0; Mismatches 273; Indels 9; Gaps 2;

normalized version of this library is also available  
 (NIH ZGC 7). Library was constructed by Open Biosystems  
 (Huntsville, AL).

Qy 137 CAGAGCCTTCCAGAGACTATGTTGGACTGAAGACCTTCAAGAGTGTCTCCACATAGCGTG 196  
 Db 50 CACAGATTACTGCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 109  
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 Db 110 TGAAGTCTCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 169  
 Qy 257 ACACAGCCAAAGTCCGCTGAGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 316  
 Db 170 ACAGGCGCAAGTCCGCTGAGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 229  
 Qy 317 TCGTCAAGTACCGTGGGCTGCTGGGACCAATCTTCAAGTGTGTGAGTGTGTGAGTGTGTGAGT 376  
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 Qy 377 GCAAGCCCTTACCAATGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGT 436  
 Db 290 GCTGCTCTACCAAGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG 349  
 Qy 437 GCATGGGCTCTATATGATCTCCGTCAGAGAGTGTATCAACCCCAAGGAGGAGGAGGAGGAGGAGG 496  
 Db 350 GATTTGGCTCTTACCAAGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGT 406  
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 Db 521 TGGGAGAGATATCAAGGAGCTATGAGAGCTTACAGAAACATTCGCCAGGAGGAGGAGGAGGAGG 580  
 Qy 677 TCAAGGAGCTGTGTAAGGAACTTTGCGCAATCATGAGAGTGTATGCTAACTGTG 736  
 Db 581 TCGGTGTCTGTGAAAGGAACTTGTCCGAAATCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 640  
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QY 1031 CCTATGAGCAGCTGAACGGGCGCTGATG 1059  
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 genomic survey sequence.  
 ACCESSION AV413338  
 VERSION AV413338.1 GI:39769300  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
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 REFERENCE 1 (bases 1 to 930)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,P., Murphy,B.,  
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submision  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 930)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,P., Murphy,B.,  
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submision  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.

TITLE JOURNAL  
 COMMENT

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 Best Local Similarity 63.9%; Pred. No. 1.5e-83;  
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QY 154 ATGGTTGAGTGAAGCTTGTAGACGTGCTCCCAACCAATGAGTGAAGTTCCTGGGGGCA 213  
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QY 214 GGCACAGCAGCTGTTTGTGCTGACCTGTTACCTTTCCACTGACACAGCCAAAGTCCG 273  
 DB 61 GGCACAGCTGCTGCTGACCTGACGATCTATCACTTTCTCTGATATGCTGAAGTCCG 120

QY 274 CTGCAATCCAGGGGGAACACAGG---CGGTCCAGACGGCCGGCTGTGCACTACCT 330  
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 DB 181 GGTGTGATGGCAGCACTTGTGACCATAGTGTGCTAGAGGCCCCCGAAGCTCTTACAT 240

QY 391 GGGCTGTGCGCCGCTGACAGCCGCAATGAGCTTCCCTTCATCCGATCGGCTCTAT 450  
 DB 241 GGGCTGTGCTGCGCCGCTGACAGCCGCAATGAGCTTCCCTTCATCCGATCGGCTCTAT 300

QY 451 GACTTCGTCAAGCAGGTGTACACCCCGCAAGCGCGGACAACTCAGCCTCACTACCCG 510

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 QY 511 ATTTGGCCGGCTGACACCAAGAGCCATGGCGGTGACCTGTGCCAGCCACAGATGTG 570  
 DB 358 NNN 417

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QY 631 AGCGGACCTATGAGAGCCCTACAGAACATTCGACAGAGAGAGAGATCAGGCGCTGTG 690  
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QY 991 TTTTTCGTTTGGGATCTGGAACGTGTGATGTTGTAACCTATGAGAGCTGAACCG 1050  
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RESULT 15  
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 mRNA sequence.  
 ACCESSION B1248501  
 VERSION B1248501.1 GI:14794652  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 927)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LLM1367 row: p column: 04  
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 Library constructed by Life Technologies. Investigators  
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 NIH"

## ORIGIN

Query Match 32.9%; Score 405.4; DB 12; Length 927;  
 Best Local Similarity 71.8%; Pred. No. 4.1e-80;  
 Matches 605; Conservative 0; Mismatches 221; Indels 17; Gaps 5;

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DB 7 GTCCGAGCTGCTGACATTCATCACTTCCCTGTGATACCGCAAGTCCGG 66
OY 274 CTGCAGATCCAGGGGAGAAACAGCGC---GTCCAGACGGCCCGGCTCTGTCACTACCT 330
DB 67 CTGCAGATCCAGGGGAGAGTCAAGGGCTAAGTCCGACCGCAGCCAGCCAGTACCGT 126
OY 331 GGGGTCTGGGGACCATCTGACCATGATGATGAGGCTTCCATCCGATCCGCTCTAT 390
DB 127 GGGGTCTGGGGTTCATCTTACCATGATGATGAGGCTTCCATCCGATCCGCTCTAT 186
OY 391 GGGGTCTGGGGCCGCTGACCGCCAGATGAGCTTCCATCCGATCCGCTCTAT 450
DB 187 GGGGTCTGGGGCCGCTGACCGCCAGATGAGCTTCCATCCGATCCGCTCTAT 246
OY 451 GACTCCGTCAAGAGGTGTACACCCCAAGGGCGGCAACTCCAGCTCACTACCCGG 510
DB 247 GACTCTGTCAACAGTCTTACA---CCAGGGCTCAGAGCATCAGGCACTGGAGCCGC 303
OY 511 ATTTTGGCGGGCTGACACAGAGGACATGGCGGTGACCTGTGCCAGCCCAAGATGT 570
DB 304 CTCTGGCAGGTACACACAGGTGCTTGGCCGTGTGATGCCCTTACAGATGTG 363
OY 571 GTGAAGTCCGATTTGAGGCAACATCACTCGGGCATCCAGAGCGACAGAAATAC 630
DB 364 GTAAAGTCCGCTTCAAGC-----TCAGGCCGGGCTGTGTGTGCGAGATAC 414
OY 631 AGCGGACATGAGACGCTTACAGACCATGCGCAGGAGGAGAGTCAAGGGCTGTGG 690
DB 415 CAGAGCATGTGCAAGCTTACAGACCATTGCAGAGAGGAGGATCCCGGGCTCTGG 474
OY 691 AAAGGAACTTTGGCCCAACATCATGAGGAATGTATGTCAACTGTGCTGAGTGTGA-C 749
DB 475 AAAGGAACTTCTCCATATGTGCGCTTATGCAATGTCACTGTGCTGAGCTGTGACC 534
OY 750 CTACGACATCTCAAGAGAGCTGTGACTTACCACTGTGCTCACTGACAACTTCCCTG 809
DB 535 CTATGACCTTATTAAGATATCTCTCTGAAGCAACCTCATGACAGATGACCTCCCTG 594
OY 810 CCACTTTGTCTGTGCTTTGAGCCCGCTTCTGTGCAAGTGTGGCTTCCCGGTGA 869
DB 595 CCACTTCACTTCTGTGCTTGGGGCCCGCTTCTGCAACGCTCATGCTCCCTGTGA 654
OY 870 CGTGTGAGAGACCGGATATGAACTCACTCCAGGCAAGTATCTAGCCCTCGACTG 929
DB 655 TGTGTGCAAGAGCAATACATGAACTCTGTGCTTGGGCACTATCAAGCCAGTCACTG 714
OY 930 TATGATAAAGATGTGAGCCCAAGAGGAGCCCAAGCCCTTCAAGGATTTACACCTC 989
DB 715 TGCCCTTACATGCTCCGAGAGGAGAGCCCGGCTTCTACAGGGGTCAATGCTTTC 774
OY 990 CTTTGTGCTTGGATCTGTGAAGTGTGATGTTGTGTAACCTATGAGCACTGAACG 1049

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DB 775 CTTTCCGCTTGGATCTGTG-ACGTAGTATGTTTGCACCTATGAGCACTGAAGA 833  
 OY 1050 GGC 1052  
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Search completed: May 18, 2004, 14:45:31  
 Job time : 3081 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

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Title: US-09-423-410-3

Perfect score: 1231  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	100.0	1231	2	AAV72690 Human unc
2	1231	100.0	1231	6	ABQ72999 Human unc
3	1202.2	97.7	2340	2	AAV84254 Human unc
4	1185.2	96.3	1220	2	AAV71710 Human unc
5	1146.4	93.1	1193	3	AAZ46055 Human unc
6	1146.4	93.1	1193	4	AAZ46055 Human unc
7	1146.4	93.1	1193	6	AAZ46055 Human unc
8	1145	93.0	1175	3	AAZ29245 Human unc
9	1144.8	93.0	1193	2	AAV54602 Human unc
10	1010.8	82.1	1032	2	AAZ08507 Human unc
11	981.4	79.7	1132	2	AAV72691 Human unc
12	981.4	79.7	1132	3	AAZ29324 Human unc
13	981.4	79.7	1132	5	AAZ14820 Human unc
14	981.4	79.7	1132	5	AAZ14820 Human unc
15	981.4	79.7	1132	6	AAZ14820 Human unc
16	967.8	78.6	1033	2	AAV71711 Human unc
17	939	76.3	939	2	AAZ19969 Human unc
18	939	76.3	939	4	AAZ19969 Human unc
19	934.4	75.9	936	5	AAZ19969 Human unc
20	732	59.5	1658	2	AAV84307 Mouse unc
21	732	59.5	2782	2	AAZ07060 Mouse unc
22	732	59.5	2782	2	AAV71227 Mouse unc
23	732	59.5	2782	3	AAZ07060 Mouse unc

24	732	59.5	2782	4	AAZ09318 Mouse unc
25	730.4	59.3	1204	2	AAV71712 Mouse unc
26	708.2	57.3	1215	9	AAZ52719 Primary r
27	705.4	57.3	1949	2	AAZ07061 Mouse unc
28	705.4	57.3	1949	2	AAV71228 Mouse unc
29	705.4	57.3	1949	3	AAZ09319 Mouse unc
30	705.4	57.3	1949	4	AAZ09319 Mouse unc
31	593.8	48.2	1777	2	AAZ07062 Mouse unc
32	593.8	48.2	1777	2	AAV71229 Mouse unc
33	593.8	48.2	1777	3	AAZ09320 Mouse unc
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35	490	39.8	1575	6	AAZ63772 Rat. seq
36	490	39.8	1575	6	AAZ63772 Rat. seq
37	490	39.8	1575	9	AAZ63772 Rat. seq
38	478.2	38.8	1612	2	AAZ58373 Toxicity-
39	478.2	38.8	1612	2	AAZ58373 Toxicity-
40	476.6	38.7	1105	2	AAZ99434 Human res
41	476.6	38.7	1105	2	AAZ99434 Human res
42	476.6	38.7	1105	3	AAZ99434 Human res
43	476.6	38.7	1105	5	AAZ99434 Human res
44	476.6	38.7	1596	2	AAZ82381 Human unc
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## ALIGNMENTS

RESULT 1	AAV72690	standard; CDNA; 1231 BP.
ID	AAV72690	standard; CDNA; 1231 BP.
XX	AAV72690;	
AC	AAV72690;	
XX	AAV72690;	
DT	22-FEB-1999	(first entry)
XX	Human uncoupling protein UCP3L encoding cDNA.	
XX	Human uncoupling protein; UCP3L; UCP3; oxidative phosphorylation;	
KW	adenosine triphosphate; mitochondria; skeletal muscle; gene therapy;	
KW	thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;	
KW	insulin sensitivity; neuromuscular disease; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PH	Key	Location/Qualifiers
FT	CDS	154..1092
FT		/tag= a
FT		/product= "UCP3L"
XX	W09850542-A1.	
XX	12-NOV-1998.	
PD	05-MAY-1998;	98WO-EP002645.
XX	07-MAY-1997;	97CH-00001072.
XX	(NOV) NOVARTIS AG.	
PA	(NOV) NOVARTIS-ERFINDUNGEN VERM GBS MBH.	
XX	Giacobino J, Muzzin P, Boss O;	
XX	WPI, 1998-610382/51.	
DR	P-PSDB; AAW83379.	
XX	New human skeletal muscle uncoupling protein UCP3L and UCP3S - useful	
PT	for controlling thermogenesis in human skeletal muscle and heart, e.g.	
PT	for treating obesity and cachexia.	
XX	Claim 1, Page 14-15; 26pp: English.	
PS	The present sequence encodes human uncoupling protein UCP3L. UCP3	
XX	uncouples oxidative phosphorylation and synthesis of adenosine	





PA (BOET/) BOETTCHER B. R.  
 PA (SLOS/) SLOSBURG E. D.  
 PA (CONN/) CONNELLY S.  
 PA (KALE/) KALEKO M.  
 PA (DESAI/) DESAI U. J.  
 PI Caplan SL, Boettcher BR, Slosberg ED, Connelly S, Kaleko M;  
 PI Desai UJ;  
 DR WPI: 2002-556735/59.  
 DR P-PSDB; ABB81610.

PT Treating condition related to elevated blood glucose levels, especially  
 PT diabetes or obesity, involves administering polynucleotide sequence  
 PT encoding glucokinase regulatory protein, to a subject.

PS Disclosure; Page 16; 42pp; English.

CC The present invention describes a method (M1) for treating a condition  
 CC related to elevated blood glucose levels, which involves administering a  
 CC polynucleotide sequence encoding a glucokinase regulatory protein (GKR),  
 CC to a subject. Also described: (1) increasing liver glucokinase (GK)  
 CC activity, by administering a polynucleotide sequence encoding GKR; and  
 CC (2) a method (M2) treating diabetes or diabetes-related condition, by  
 CC administering to a subject, one or more metabolism modifying proteins and  
 CC peptides in combination with GK or GKR, or their combination. (M1) and  
 CC (M2) can be used for treating diabetes (type I and II diabetes) or  
 CC diabetes-related conditions such as obesity, increased hepatic  
 CC triglyceride accumulation, reduced hepatic fatty acid oxidation,  
 CC increased fibrinogen levels, decreased apo A-I levels, decreased high  
 CC density lipoprotein (HDL) cholesterol levels and decreased hepatic  
 CC glucose utilization. The methods are also useful for treating gestational  
 CC diabetes, hyperglycaemic related disorders such as increased cholesterol,  
 CC kidney related disorders and cardiovascular disorders. The methods  
 CC overcome a limitation to the over-expression of GK in the liver which  
 CC usually increases liver size and hepatic fat accumulation in normal and  
 CC diabetic mice. The present sequence encodes a UCP3L protein which is  
 CC given in the exemplification of the present invention

CC Sequence 1231 BP; 271 A; 371 C; 345 G; 244 T; 0 U; 0 Other;

Query Match 100.0%; Score 1231; DB 6; Length 1231;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-295;  
 Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGGAGTGAAGCCCTTGAAGAGCCCTTGTCTGCCCTGCGTGGCAGAGTCAAGGCC 60  
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 Db 61 CCAACGCTGCTGAGAGCCCAAGGCTGTGGAGAGAGCTCTCTCTTGAAGCTCTCTCGG 120  
 QY 121 CCTTAAGGAGTGGGCAAGAGCTTCAAGAGCTATGTTGAGCTGAAGCTTCAAGCGTG 180  
 Db 121 CCTTAAGGAGTGGGCAAGAGCTTCAAGAGCTATGTTGAGCTGAAGCTTCAAGCGTG 180  
 QY 181 CCTCCCAACATGAGCTGTGAAGTCTGTGGGGCAGGACAGCAGCTCTTTTGTGACTTC 240  
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 Db 961 ACAAGCTTTTAAAGAGGATTTTACACCTCTTTTGGGTTGGGATCTGGAACGTTG 1020  
 QY 1021 ATGTTGTTAACTATGAGAGCTGTAACCGGCTCTGATGAAAGTGTATGTTACCGGAA 1080  
 Db 1021 ATGTTGTTAACTATGAGAGCTGTAACCGGCTCTGATGAAAGTGTATGTTACCGGAA 1080  
 QY 1081 TCACGTTTGTGAACAAGAAAGGCCACTGTGACTTAAAGTGTCCGAAACCAAGTTAAG 1140  
 Db 1141 TCACGTTTGTGAACAAGAAAGGCCACTGTGACTTAAAGTGTCCGAAACCAAGTTAAG 1140  
 QY 1141 AATGAAAGAAACGGTGATTCACAGCAACATGGAACAAGACCAATGTTTACAGAA 1200  
 Db 1141 AATGAAAGAAACGGTGATTCACAGCAACATGGAACAAGACCAATGTTTACAGAA 1200  
 QY 1201 CTGTTGTTACTTGTGCTGATTCAGAAAC 1231  
 Db 1201 CTGTTGTTACTTGTGCTGATTCAGAAAC 1231

RESULT 3  
 ID AAV84254  
 AA84254 standard; cDNA; 2340 BP.  
 XX AAV84254;  
 AC  
 XX  
 XX  
 DT 12-APR-1999 (first entry)  
 XX  
 XX  
 DE Human uncoupling protein 3 (UCP3) cDNA.  
 XX  
 KM Uncoupling protein 3; UCP3; human; obesity; diabetes; hyperinsulinaemia;  
 XX hypermetabolism; gene therapy; ds.  
 OS  
 XX Homo sapiens.  
 FH  
 Key Location/Qualifiers

FT CDS 344, .1282  
 FT /\*tag= a  
 FT /note= "this region is specifically claimed in Claim 2"  
 XX MO9852958-A1.  
 XX 26-NOV-1998.  
 XX 19-MAY-1998; 98WO-US010215.  
 XX 20-MAY-1997; 97US-0047179P.  
 XX 08-AUG-1997; 97GB-00016886.  
 XX 09-DEC-1997; 97US-0069141P.  
 XX (MERI ) MERCK & CO INC.  
 XX Liu Q, Chen F;  
 XX WPI, 1999-059737/05.  
 XX P-PSDB; AAW88279.  
 PT New isolated human uncoupling protein 3 - used to identify compounds  
 PT which can modulate energy expenditure and body weight regulation, e.g. in  
 PT the treatment of obesity or diabetes.  
 XX Claim 1; Page 57-58; 87P; English.  
 CC This cDNA clone encodes human uncoupling protein 3 (UCP3, see AAW88279),  
 CC a novel protein that is involved in energy expenditure and body weight  
 CC regulation and whose expression is mostly limited to skeletal muscle. The  
 CC clone was isolated from a foetal brain cDNA library using primers (see  
 CC AAW84259-54) based on isolated EST clones (see AAW84255-58) and  
 CC pBluescript vector sequences. The invention additionally provides related  
 CC recombinant expression vectors, recombinant host cells and purified forms  
 CC of the UCP3 protein. The UCP3 polypeptides and transformed recombinant  
 CC cell lines can be used for identifying modulators of UCP3 activity. Such  
 CC modulators can be used for treating diseases such as obesity and  
 CC diabetes, by manipulating the interrelated process of balancing food  
 CC intake, energy expenditure and glucose metabolism within the patient.  
 CC They can also be used to treat hyperactive conditions of energy  
 CC expenditure which originate in the mitochondria of skeletal muscle. UCP3  
 CC nucleic acids are useful in gene therapy of obesity and obesity-related  
 CC indications, including diabetes, and of mitochondrial-associated  
 CC hypermetabolism  
 CC  
 CC Sequence 2340 BP; 606 A; 638 C; 633 G; 463 T; 0 U; 0 Other;  
 SO  
 Query Match 97.7%; Score 1202.2; DB 2; Length 2340;  
 Best Local Similarity 99.6%; Pred. No. 5.9e-288;  
 Matches 1226; Conservative 0; Mismatches 3; Indels 2; Gaps 2;  
 QY 1 TCCTGGATGAGCCCTGAGGAGCCCTGCTGCTGCCCCCTGAGCAGAGCTCAAGCC 60  
 DB 193 TCCTGGATGAGCCCTGAGGAGCCCTGCTGCTGCCCCCTGAGCAGAGCTCAAGCC 252  
 QY 61 CCACCGCTGCACTGAGAGCCCAAGGCTGTGAGCAGAGCTCTCTCTGAGCCTCTGCG 120  
 DB 253 CCACCGCTGCACTGAGAGCCCAAGGCTGTGAGAG-CTCTCTCTGAG-CTCTCTGCG 310  
 QY 121 CCTTAAAGGAGCTGGGAGAGCCCTTCAGAGACTATGTTGAGCTGAGAGCTTCAAGCTG 180  
 DB 311 CCTTAAAGGAGCTGGGAGAGCCCTTCAGAGACTATGTTGAGCTGAGAGCTTCAAGCTG 370  
 QY 181 CCTCCACCATGCTGTGTAAGTTCTGGGGGAGGAGCAGAGCCCTGTTTGTGACTC 240  
 DB 371 CCTCCACCATGCTGTGTAAGTTCTGGGGGAGGAGCAGAGCCCTGTTTGTGACTC 430  
 QY 241 GTTACTTTTCACTGAGCAGAGCAGAGCTCGCTGCAATTCAGAGGAGGAGAAACAAGCG 300  
 DB 431 GTTACTTTTCACTGAGCAGAGCAGAGCTCGCTGCAATTCAGAGGAGGAGAAACAAGCG 490  
 QY 301 GTTCAAGAGGCGGCTGCTGAGTACCTGCTGCTGCTGAGCAATCTTCAAGCAATGCTG 360

DB 491 GTCCAGAGCGCCCGGCTGTGAGTACCTGTGCTGTGAGCAACCATCTGACATGATG 550  
 QY 361 CGAGTGAAGGCTCTGACAGCCCTTCAATAGGCTGTGTGCTGCGGCTGTGACGCGCAATG 420  
 DB 551 CGAGTGAAGGCTCTGACAGCCCTTCAATAGGCTGTGTGCTGCGGCTGTGACGCGCAATG 610  
 QY 421 AGCTTGGCTCTCAATCCGATCCGAGTCTATGAGTCCGTCAGAGAGTGTACACCCCAAA 480  
 DB 611 AGCTTGGCTCTCAATCCGATCCGAGTCTATGAGTCCGTCAGAGAGTGTACACCCCAAA 670  
 QY 481 GCGCGGAGCAATCTGACCTCACTACCCGAGATTTTGGCCGCTGACCAAGAGCCATG 540  
 DB 671 GCGCGGAGCAATCTGACCTCACTACCCGAGATTTTGGCCGCTGACCAAGAGCCATG 730  
 QY 541 GCGGTGACTGTGCTGAGCCCAAGATGTGTGAGTCCGATTTCAAGCCATAC 600  
 DB 731 GCGGTGACTGTGCTGAGCCCAAGATGTGTGAGTCCGATTTCAAGCCATAC 790  
 QY 601 CTGGGCTATTCAGAGAGCAGAGAAATACAGCGGAGCTATGAGCGCTTACAGAACATC 660  
 DB 791 CTGGGCTATTCAGAGAGCAGAGAAATACAGCGGAGCTATGAGCGCTTACAGAACATC 850  
 QY 661 GCCAGGAGAGAGAGTCAAGGAGCTGTGAGAAAGAACTTTGCCCAATCATAGAGAT 720  
 DB 851 GCCAGGAGAGAGAGTCAAGGAGCTGTGAGAAAGAACTTTGCCCAATCATAGAGAT 910  
 QY 721 GCTATCTGCACTGTGCTGAGAGTGTGCTTACAGATCTTCAAGAGAACTGTGAG 780  
 DB 911 GCTATCTGCACTGTGCTGAGAGTGTGCTTACAGATCTTCAAGAGAACTGTGAG 970  
 QY 781 TATGACCTGCTCACTGAGAACTTCCCTGCACTTTGCTGTGCTTGTGAGCGGCTTC 840  
 DB 971 TATGACCTGCTCACTGAGAACTTCCCTGCACTTTGCTGTGCTTGTGAGCGGCTTC 1030  
 QY 841 TGTGCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 DB 1031 TGTGCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1090  
 QY 901 CCAGGCTGATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 DB 1091 CCAGGCTGATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1150  
 QY 961 ACAGCTTCTCAAGGAGTATTAACCTCTTTTGGCTTGGAGTCTGGAACGTGTG 1020  
 DB 1151 ACAGCTTCTCAAGGAGTATTAACCTCTTTTGGCTTGGAGTCTGGAACGTGTG 1210  
 QY 1021 ATGTTGCTATGAGCAGCTGAAAGGAGCCCTGATGAAAGTCCAGATGTTACGGGAA 1080  
 DB 1211 ATGTTGCTATGAGCAGCTGAAAGGAGCCCTGATGAAAGTCCAGATGTTACGGGAA 1270  
 QY 1081 TCACGTTTGAACAAGCAAGAAAGGCACTGTGATCTTACGCTGCTGGAACCACTTAA 1140  
 DB 1271 TCACGTTTGAACAAGCAAGAAAGGCACTGTGATCTTACGCTGCTGGAACCACTTAA 1330  
 QY 1141 AATGGAAGAAAGCTGTGATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1200  
 DB 1331 AATGGAAGAAAGCTGTGATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1390  
 QY 1201 CTGTTGTTTACTGTTGCTGATTCAGAAAC 1231  
 DB 1391 CTGTTGTTTACTGTTGCTGATTCAGAAAC 1421  
 RESULT 4  
 AA71710  
 ID AA71710 standard; DNA; 1220 BP.  
 XX AA71710;  
 AC 09-FEB-1999 (first entry)  
 XX Human uncoupling protein 3 (UCP3) encoding DNA.  
 DE  
 XX



QY 1141 AATGAGAGAAAACGGTGCATCCACGACACATGACACAGACCCACACAT 1190  
 DB 1171 AATGAGAGAAAACGGTGCATCCACGACACATGACACAGACCCACACAT 1220

RESULT 5  
 AA246055  
 ID AA246055 standard; cDNA; 1193 BP.

XX AA246055;

XX 25-APR-2000 (first entry)

XX cDNA encoding a human uncoupling protein designated HHFCW60.

XX Human; HHFCW60; mitochondrial uncoupling protein family; muscle wasting;

XX uncoupling protein; wound; tissue repair; inflammation; cachexia; 88.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 199..1137

XX /tag= a

XX /product= "uncoupling protein"

XX MO200002577-A1.

XX 20-JAN-2000.

XX 02-DEC-1998; 98WO-EP007802.

XX 09-JUL-1998; 98GB-00014926.

XX (SMK ) SMITHKLINE BEECHAM PLC.

XX Clapham JC, Beeley LJ, Godden RJ;

XX WPI; 2000-147542/13.

XX P-PsDB; AAY54600.

XX Use of uncoupling protein, polynucleotide and compound activating it, in

XX treating wounds, inflammation, tissue repair, muscle wasting, and

XX cachexia.

XX Claim 9; Page 21; 29pp; English.

XX The present sequence encodes a HHFCW60 polypeptide, which is a member of

XX the mitochondrial uncoupling protein family. The HHFCW60 polynucleotide

XX has homology with human uncoupling protein 2. The polynucleotide sequence

XX was isolated from a cDNA library derived from human skeletal muscle cell

XX mRNA, and mRNA from the cell lines rhabdomyosarcoma, caski, and SH-SY 5Y. The

XX protein is useful in producing antibodies and in screening for antagonist

XX and agonist. The polynucleotide is useful as a reagent for diagnosing and

XX determining susceptibility to the disease by detecting the mutation in

XX the HHFCW60 gene. The polynucleotide, protein, and antibodies against

XX HHFCW60 are useful in screening for the compounds that have an effect on

XX the production of mRNA and polypeptides in the cell. These compounds are

XX used to treat wounds, tissue repair, inflammation, muscle wasting or

XX cachexia

Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;

Query Match 93.1%; Score 1146.4; DB 3; Length 1193;

Best Local Similarity 99.9%; Pred. No. 3.3e-274;

Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTTGGATGAGAGCCCTAGAGAGCCCTGTGCTGCTCCCTGTCAGAGACTCAGAGCC 60

DB 46 TCTTGGATGAGAGCCCTAGAGAGCCCTGTGCTGCTCCCTGTCAGAGACTCAGAGCC 105

QY 61 CCACCGCTGCACTGAAGCCAGGAGCTGTGAGAGAGCTCTCTCTTGAAGCTCTCTCGG 120

DB 106 CCACCGCTGCACTGAAGCCAGGAGCTGTGAGAGAGCTCTCTCTTGAAGCTCTCTCGG 165

QY 121 CCTAAAGGAGCTGGGAGAGAGCTTCCAGAGACTATGTTGAGTGAAGCTTCAAGCTG 180

DB 166 CCTAAAGGAGCTGGGAGAGAGCTTCCAGAGACTATGTTGAGTGAAGCTTCAAGCTG 225

QY 181 CTTCCACACATGCTGTGAAGTTCTTGGGGGAGAGACAGAGCTGTTTGGTGAAGCTC 240

DB 226 CTTCCACACATGCTGTGAAGTTCTTGGGGGAGAGACAGAGCTGTTTGGTGAAGCTC 285

QY 241 GTTACCTTTCACTGAGACAGAGAGAGTCCGCTGAGATCCAGGGGAGAGACAGAGCG 300

DB 286 GTTACCTTTCACTGAGACAGAGAGAGTCCGCTGAGATCCAGGGGAGAGACAGAGCG 345

QY 301 GTCCAGAGGAGCCGAGCTGTGTCAGTACCGTGGAGCTGTGAGACCATCTTGAAGCTG 360

DB 346 GTCCAGAGGAGCCGAGCTGTGTCAGTACCGTGGAGCTGTGAGACCATCTTGAAGCTG 405

QY 361 CGAAGTGAAGGTTCTTGAAGCTTCAATGAGGCTGTGAGGCTGAGGCTGAGGAGAGT 420

DB 406 CGAAGTGAAGGTTCTTGAAGCTTCAATGAGGCTGTGAGGCTGAGGCTGAGGAGAGT 465

QY 421 AGCTTGGCTGCTCATCCGATGAGGCTGTGATGATCCGCTCAAGAGAGTGAACCCCAAA 480

DB 466 AGCTTGGCTGCTCATCCGATGAGGCTGTGATGATCCGCTCAAGAGAGTGAACCCCAAA 525

QY 481 GAGCGGAGCAACTCCAGAGCTGACTAACCCGAGATTTTGGCCGAGCTGACCAAGAGCCATG 540

DB 526 GAGCGGAGCAACTCCAGAGCTGACTAACCCGAGATTTTGGCCGAGCTGACCAAGAGCCATG 585

QY 541 GGGGTGACCTGTGCTGAGAGCCCAAGATGATGATGATGATGATGATGATGATGATGAT 600

DB 586 GGGGTGACCTGTGCTGAGAGCCCAAGATGATGATGATGATGATGATGATGATGATGAT 645

QY 601 CTGGGAGCAACTCCAGAGCTGACTAACCCGAGATTTTGGCCGAGCTGACCAAGAGCCATG 660

DB 646 CTGGGAGCAACTCCAGAGCTGACTAACCCGAGATTTTGGCCGAGCTGACCAAGAGCCATG 705

QY 661 GCGAGGAGAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

DB 706 GCGAGGAGAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765

QY 721 GCTATGCTCACTGCTGAGAGTGTGAGCTTACAGACATCTCTCAAGAGAGAGTGTGAGC 780

DB 766 GCTATGCTCACTGCTGAGAGTGTGAGCTTACAGACATCTCTCAAGAGAGAGTGTGAGC 825

QY 781 TACCACTGCTCACTGAGACACTTCCCTGAGCACTTGTCTCTGCTTGGAGCCGAGCTTC 840

DB 826 TACCACTGCTCACTGAGACACTTCCCTGAGCACTTGTCTCTGCTTGGAGCCGAGCTTC 885

QY 841 TGTGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 900

DB 886 TGTGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 945

QY 901 CCAAGGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 960

DB 946 CCAAGGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1005

QY 961 ACAGGCTTCAAGAGAGATTTTCAAGCTTCTTGTGCTTGTGAGTGTGAGTGTGAGTGTGAGT 1020

DB 1006 ACAGGCTTCAAGAGAGATTTTCAAGCTTCTTGTGCTTGTGAGTGTGAGTGTGAGTGTGAGT 1065

QY 1021 ATGTTGTAACCTATGAGAGAGTGAAGAGGAGCTGTGATGAAGTCAAGTGTGAGAGAA 1080

DB 1066 ATGTTGTAACCTATGAGAGAGTGAAGAGGAGCTGTGATGAAGTCAAGTGTGAGAGAA 1125

QY 1081 TCAAGCTTTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGTAA 1140

DB 1126 TCAAGCTTTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGTAA 1185

QY 1141 AATGAGAG 1148

DB 1186 AATGAGAG 1193

## RESULT 6

AAD08530 standard; cDNA; 1193 BP.

AAD08530;

04-SEP-2001 (first entry)

Human uncoupling protein-3 (UCP3) cDNA.

Human; UCP3; uncoupling protein-3; chromosome 11q13; gene therapy; atherosclerosis; hypercholesterolemia; antilipemic; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 199..1137

FT /product= "Human UCP3 protein"

FT 21-JUN-2001.

FT 18-DEC-2000; 2000MO-BP012931.

FT 17-DEC-1999; 99GB-00030100.

(SMIT ) SMITHKLINE BEECHAM PLC.

Clapham JC;

WPI: 2001-398073/42.

P-PSDB; AAE04298.

Use of a compound selected from UCP3 polypeptide, a compound which activates the polypeptide, or a polynucleotide encoding the polypeptide, for treating atherosclerosis or hypercholesterolemia.

Claim 9; Page 19; 24pp; English.

The present sequence is a cDNA encoding human UCP3 (uncoupling protein-3) protein. UCP3 gene is located in chromosome 11q13. UCP3 protein and polynucleotides encoding them are useful for identifying agonist compounds which are potentially useful in therapy. UCP3 protein is useful for inducing an immunological response, as immunogen to produce antibodies immunospecific for UCP3 protein, and in a method for the structure-based design of an agonist of UCP3 protein. UCP3 sequences are useful to configure screening methods for detecting the effect of added components on the production of mRNA and polypeptide in cells. UCP3 DNA is used in gene therapy. A compound which activates UCP3 protein or a polynucleotide encoding UCP3 protein are used for the manufacture of a medicament for treating atherosclerosis or hypercholesterolemia

Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;

Query Match 93.1%; Score 1146.4; DB 4; Length 1193;

Best Local Similarity 99.9%; Pred. No. 3.3e-274; Indels 0; Gaps 0;

Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCTGGATGAGACCTTAGGAGCCCTGTGCTGCCCTGCGTGAGAGCTACAGCC 60

46 TCTTGGATGAGACCTTAGGAGCCCTGTGCTGCCCTGCGTGAGAGCTACAGCC 105

61 CCAAGCGCTGAGAGCCAGGAGCTGTGAGAGAGCTCTCTTGGAGCTCTCTCGG 120

106 CCACCGCTGAGAGCCAGGAGCTGTGAGAGAGCTCTCTTGGAGCTCTCTCGG 165

121 CCTTAAGGAGAGCTGGAGAGAGCTTCCAGAGCTATGTTGAGAGTGAAGCTTGAAG 180

166 CCTTAAGGAGAGCTGGAGAGAGCTTCCAGAGCTATGTTGAGAGTGAAGCTTGAAG 225

181 CTCCACCATAGCTGTGAGAGTTCTTGGGGGAGGAGAGAGAGCTGTTTGTGACCTC 240

226 CTCCACCATAGCTGTGAGAGTTCTTGGGGGAGGAGAGAGCTGTTTGTGACCTC 285

241 GTTACCTTTCATGAG 300

286 GTTACCTTTCATGAG 345

301 GTTACAG 360

346 GTTACAG 405

361 CGAGTGAAG 420

406 CGAGTGAAG 465

421 AGCTTGGAG 480

466 AGCTTGGAG 525

481 GGGGAG 540

526 GGGGAG 585

541 GGGGAG 600

586 GGGGAG 645

601 CTGGGAG 660

646 CTGGGAG 705

661 GCGAG 720

706 GCGAG 765

721 GCTATGCTGAG 780

766 GCTATGCTGAG 825

781 TACAG 840

826 TACAG 885

841 TGTGAG 900

886 TGTGAG 945

901 CCAAG 960

946 CCAAG 1005

961 ACAAG 1020

1006 ACAAG 1065

1021 ATGTTGAG 1080

1066 ATGTTGAG 1125

1081 TCAAG 1140

1126 TCAAG 1185

1141 AATGAGAG 1148

1186 AATGAGAG 1193

RESULT 7

AAD30499 standard; cDNA; 1193 BP.

AAD30499



AC AAD0499;  
 XX 31-MAY-2002 (first entry)  
 DT  
 XX Human mitochondrial uncoupling protein 3 (UCP3) cDNA.  
 DE  
 XX Human; mitochondrial uncoupling protein 3; UCP3; obesity; diabetes;  
 XX body weight disorder; gene therapy; chromosome 11q13; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 199.1137  
 FT CDS /tag=a  
 FT /product="Human UCP3 protein"  
 FT  
 PN W020020754-A2.  
 PD 31-JAN-2002.  
 PE 25-JUL-2001; 2001WO-GB003341.  
 XX  
 XX 25-JUL-2000; 2000GB-00018248.  
 XX  
 XX (SMK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Clapham J;  
 PI  
 DR WPI; 2002-217023/27.  
 DR P-Psdb; AAE19348.  
 XX  
 XX  
 PT Use of mitochondrial uncoupling protein 3 polypeptide, polynucleotide and  
 PT compounds which activate the polypeptide or polynucleotide for treating  
 PT obesity, diabetes or body weight disorder.  
 PS  
 XX Claim 9; Page 18; 22pp; English.  
 CC The present sequence is human mitochondrial uncoupling protein 3 (UCP3)  
 CC encoding cDNA. The UCP3 gene is located on chromosome 11q13. UCP3  
 CC sequences are used for identifying compounds which modulate their  
 CC activity. They are used for the manufacture of a medicament for treating  
 CC obesity, diabetes and body weight disorder. UCP3 sequences are also used  
 CC in gene therapy  
 CC  
 SQ Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;  
 Query Match 93.1%; Score 1146.4; DB 6; Length 1193;  
 Best Local Similarity 99.9%; Pred. No. 3.3e-274;  
 Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 361 CGACTGAGGATCCCTGACGCCCCCTAACAATGGCTGTGGCCGCGCTGACGCAAGATG 420  
 DB 406 CGACTGAGGATCCCTGACGCCCCCTAACAATGGCTGTGGCCGCGCTGACGCAAGATG 465  
 QY 421 AGCTTGGCTTCATCCGCAATGAGCTCTATGACTCCGTAAGAGAGGTGTACACCCCAAA 480  
 DB 466 AGCTTGGCTTCATCCGCAATGAGCTCTATGACTCCGTAAGAGAGGTGTACACCCCAAA 525  
 QY 481 GCGCGGGAACAATCAGCTCACTACCCGGAATTTTGGCCGCTGACCAACAGAGCCATG 540  
 DB 526 GCGCGGGAACAATCAGCTCACTACCCGGAATTTTGGCCGCTGACCAACAGAGCCATG 585  
 QY 541 GCGGTGACCTGTGGCCGCAAGCCCAAGATGTGTGAAGGTCGATTTCAAGCCAGATACAC 600  
 DB 586 GCGGTGACCTGTGGCCGCAAGCCCAAGATGTGTGAAGGTCGATTTCAAGCCAGATACAC 645  
 QY 601 CTCGGGCCATCAGAGAGGACAGAAAATACAGCGGGAATATGAGCGCTTACAGAACATC 660  
 DB 646 CTCGGGCCATCAGAGAGGACAGAAAATACAGCGGGAATATGAGCGCTTACAGAACATC 705  
 QY 661 GCCAGGAGAGAGAGATGAGGGGCTGTGAGAAAGAACTTTGGCCCAATGATGAGAAAT 720  
 DB 706 GCCAGGAGAGAGAGATGAGGGGCTGTGAGAAAGAACTTTGGCCCAATGATGAGAAAT 765  
 QY 721 GCTATCGTCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 DB 766 GCTATCGTCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 825  
 QY 781 TACCACTGCTCACTGACCAATCTCCCTGCACTTTGCTCTGCTTTGAGCCGCTTC 840  
 DB 826 TACCACTGCTCACTGACCAATCTCCCTGCACTTTGCTCTGCTTTGAGCCGCTTC 885  
 QY 841 TGTGCAAGATGTGTGCTCCCGGATGAGCTGTGTGAGAGACCCGATATATGATCACT 900  
 DB 886 TGTGCAAGATGTGTGCTCCCGGATGAGCTGTGTGAGAGACCCGATATATGATCACT 945  
 QY 901 CCAGGCGAGTACTCAGGCCCCCTGACTGTATGATGATGATGATGATGATGATGATGATG 960  
 DB 946 CCAGGCGAGTACTCAGGCCCCCTGACTGTATGATGATGATGATGATGATGATGATGATG 1005  
 QY 961 ACAAGCTTCTCAAGAGATTTTACACCTCTTTTGGCTTTGGATCTCTGAACTGTGTG 1020  
 DB 1006 ACAAGCTTCTCAAGAGATTTTACACCTCTTTTGGCTTTGGATCTCTGAACTGTGTG 1065  
 QY 1021 ATGTTCTGTAACCTATGAGCACTGAAAGGGCCCTGAGGAAGTCAAGTATGAGGAA 1080  
 DB 1066 ATGTTCTGTAACCTATGAGCACTGAAAGGGCCCTGAGGAAGTCAAGTATGAGGAA 1125  
 QY 1081 TCACCGTTTGAACAAGACAAGAGGCACTGTGTGATGATGATGATGATGATGATGATG 1140  
 DB 1126 TCACCGTTTGAACAAGACAAGAGGCACTGTGTGATGATGATGATGATGATGATGATG 1185  
 QY 1141 AATGGAAG 1148  
 DB 1186 AATGGAAG 1193

RESULT 8  
 AA229245  
 ID AA229245 standard; cDNA, 1175 BP.  
 XX  
 XX AA229245;  
 XX  
 XX 28-FEB-2000 (first entry)  
 DT  
 XX Human mitochondrial anion carrier, uncoupling protein-3 cDNA.  
 DE  
 XX Mitochondrial uncoupling protein-3; UCP-3; mitochondrial anion carrier;  
 XX MAC; modulator; transport protein; fatty acid anion; mitochondria;  
 XX assay vesicle; metabolic disorder; diabetes; obesity; cancer; human; de.  
 OS Homo sapiens.





XX PF 25-MAR-1998; 98WO-US005892.  
 XX PR 04-APR-1997; 97US-0043407P.  
 XX PR 08-MAY-1997; 97US-0046154P.  
 XX PA (AMYL-) AMYLIN PHARM INC.  
 XX PI Larkin S, Moore C, Albrandt K, Young A, Beaumont K;  
 XX WPI: 1999-131682/11.  
 XX P-PSDB; AAM85667.  
 XX PT New isolated uncoupling protein, UCP3 - used to develop products for  
 XX PT modulating thermogenesis in tissues, e.g. for treating obesity, diabetes,  
 XX PT malignant hyperthermia or fever.  
 XX PS Claim 5; Fig 5; 97pp; English.  
 XX CC The uncoupling protein UCP-3 is involved in thermogenesis and energy  
 XX CC utilization in skeletal muscle. The nucleic acid molecule encoding UCP-3  
 XX CC or compounds which activate UCP-3 can be used to increase thermogenesis  
 XX CC in a subject, e.g. for treating obesity or for decreasing the amount of  
 XX CC fat in a subject. They can also be used for treating diabetes. Compounds  
 XX CC which inhibit UCP-3 activation in tissues of a subject can be used for  
 XX CC decreasing thermogenesis or respiratory ATP synthesis e.g. for preventing  
 XX CC or treating malignant hyperthermia or fever. The UCP-3 can also be used  
 XX CC for screening for compounds that bind to or modulate the activity of UCP-  
 XX CC 3, these compounds can then be used in detection and diagnosis  
 SQ Sequence 1022 BP; 228 A; 301 C; 292 G; 201 T; 0 U; 0 Other;

Query Match 82.1%; Score 1010.8; DB 2; Length 1022;  
 Best Local Similarity 99.8%; Pred. No. 1.3e-240;  
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 GGCAGAGCCTTCAGAGCTATGTTGAGTGAAGCTTCAGAGCTTCACCATGCG 194  
 DB 9 GGCAGAGCCTTCAGAGCTATGTTGAGTGAAGCTTCAGAGCTTCACCATGCG 68  
 QY 195 TGTGAAGTTCCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254  
 DB 69 TGTGAAGTTCCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 128  
 QY 255 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 314  
 DB 129 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 188  
 QY 315 GCTGTGAGTACGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 374  
 DB 189 GCTGTGAGTACGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248  
 QY 375 CTGACAGGCTTCAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434  
 DB 249 CTGACAGGCTTCAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 308  
 QY 435 CCGCATGAGCTTCATGATCCGCTCAAGAGAGTGTACACCCCAAGAGAGGAGGAGGAG 494  
 DB 309 CCGCATGAGCTTCATGATCCGCTCAAGAGAGTGTACACCCCAAGAGAGGAGGAGG 368  
 QY 495 GAGCTTCACTACCGGATTTTGGCCGCTGACACAGAGAGGAGGAGGAGGAGGAGGAG 554  
 DB 369 GAGCTTCACTACCGGATTTTGGCCGCTGACACAGAGAGGAGGAGGAGGAGGAGGAG 428  
 QY 555 CCAAGCCCAAGATGTGTGAAGGTCGATTTCAGGAGGAGGAGGAGGAGGAGGAGGAG 614  
 DB 429 CCAAGCCCAAGATGTGTGAAGGTCGATTTCAGGAGGAGGAGGAGGAGGAGGAGGAG 488  
 QY 615 GAGCCGACAGAAATATACAGCGGAGCTATGAGCGCTTACAGAGAGGAGGAGGAGGAG 674  
 DB 489 GAGCCGACAGAAATATACAGCGGAGCTATGAGCGCTTACAGAGAGGAGGAGGAGGAG 548  
 QY 675 AGTCAGGGGCTGTGAGAAAGAACTTTGCCCAACATCATGAGAGATCTATCGTCAACTG 734

DB 549 AGTCAGGGGCTGTGAGAAAGAACTTTGCCCAACATCATGAGAGATCTATCGTCAACTG 608  
 QY 735 TGTGAGAGTGTGAGACCTTACAGATCTTCAGAGAGAGGAGTGTGAGTACCACTGCTCAC 794  
 DB 609 TGTGAGAGTGTGAGACCTTACAGATCTTCAGAGAGAGGAGTGTGAGTACCACTGCTCAC 668  
 QY 795 TGACAACTTCCCTGACACTTGTCTCTGCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAG 854  
 DB 669 TGACAACTTCCCTGACACTTGTCTCTGCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAG 728  
 QY 855 GGCCTCCCGGAGTGTGAGAGAGCCGCTATATGATCACTTCAGAGGAGGAGTGTGAGTGT 914  
 DB 729 GGCCTCCCGGAGTGTGAGAGAGCCGCTATATGATCACTTCAGAGGAGGAGTGTGAGTGT 788  
 QY 915 CAGCCCCCTGAGCTATGATATGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 974  
 DB 789 CAGCCCCCTGAGCTATGATATGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 848  
 QY 975 GGGATTTACACCTCTCTTTTGGGTTGGGATTCCTGGAACGTGTGATGTTGCTAACCTTA 1034  
 DB 849 GGGATTTACACCTCTCTTTTGGGTTGGGATTCCTGGAACGTGTGATGTTGCTAACCTTA 908  
 QY 1035 TGAGAGCTGAAACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1094  
 DB 909 TGAGAGCTGAAACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 968  
 QY 1095 AAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1148  
 DB 969 AAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022

## RESULT 11

AAV72691  
 ID AAV72691 standard; cDNA; 1132 BP.

AC AAV72691;

DT 22-FEB-1999 (first entry)

DE Human uncoupling protein UCP3s encoding cDNA.

KW Human, uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation;  
 KW adenine triphosphate; mitochondria; skeletal muscle; gene therapy;  
 KW thermogenesis; heart; obesity; cachexia; type II diabetes; hyperextension;  
 KW insulin sensitivity; neuromuscular disease; ss.

OS Homo sapiens.

Key Location/Qualifiers  
 CDS 154..991  
 FT /\*tag= a  
 FT /product= "UCP3s"

PN W09850542-A1.

PD 12-NOV-1998.

PF 05-MAY-1998; 98WO-EP002645.

PR 07-MAY-1997; 97CH-00001072.

PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERM GES MBH.

PI Giacobino J, Muzzin P, Boss O;

DR WPI: 1998-610362/51.

DR P-PSDB; AAM83380.

PT New human skeletal muscle uncoupling proteins UCP3L and UCP3S - useful  
 PT for controlling thermogenesis in human skeletal muscle and heart, e.g.  
 PT for treating obesity and cachexia.

XX Claim 3; Page 17-18; 26pp; English.  
PS

XX Claim 3, Page 17-18; 26pp; English.

XX

XX

CC The present sequence encodes human uncoupling protein UCP3. UCP3

CC uncouples oxidative phosphorylation and synthesis of adenosine

CC triphosphate in the mitochondria of skeletal muscle. The coding sequences

CC for UCP3L and UCP3S are useful for gene therapy of dysfunctions of

CC thermogenesis in human skeletal muscle and heart which result from a lack

CC of UCP3 and which can induce disorders such as obesity or cachexia.

CC Antisense oligonucleotides to UCP3L and UCP3S can be used for correcting

CC an excess of UCP3. Modification of endogenous UCP3 activity (using

CC activators or inhibitors of UCP3) is used to induce bodyweight loss (loss

CC of adipose mass and maintenance of the lean mass) in all types of obesity

CC by promoting the dissipation of energy; for preventing an excessive

CC weight regain following restrictive food diet or after ceasing a physical

CC training programme; for preventing and treating type II diabetes by

CC improving sensitivity to insulin; for preventing hypertension; for

CC increasing muscle mass in states of cachexia; for treatment of

CC insufficiencies or disturbances of cardiac rhythm due to a dysfunction of

CC UCP3; and for the treatment of neuromuscular diseases due to a

CC dysfunction of UCP3. The uncoupling proteins can also be used to raise

CC antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows

CC generation of transgenic animals, e.g. for screening substances which

CC modify UCP3 expression or activity or for investigating the biological

CC role of UCP3

XX

XX

SQ Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;

Query Match	79.7%;	Score 981.4;	DB 2;	Length 1132;
Best Local Similarity	99.4%;	Pred. NO. 2.7e-233;		
Matches 985; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0

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Best Local Samtality: 22.78; 12.00; 22.00;
Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Best Local Samtality      22.78%      12.00%      22.00%
Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0

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Db 601 CTGCGGCGCATCCAGGAGCGACAGAAAATAACAGCGGGACTATGACGCGCTTACAGAACCATC 666

Oy 661 GCCAGGGAGGAAGAGATCAGGGGCTGTGGAAAGAACTTTGCCAATCATAGAGAT 720

Db 661 GCCAGGGAGGAAGAGATCAGGGGCTGTGGAAAGAACTTTGCCAATCATAGAGAT 720

Oy 721 GCTATGTCACACTGTGCTGAGGTGGATCTACGACATCTCAAGSAGAACTCTGAC 780

Db 721 GCTATGTCACACTGTGCTGAGGTGGATCTACGACATCTCAAGSAGAACTCTGAC 780

Oy 781 TACCACTGCTCACTGACAACTTCCCTGCCATTGTCTGCTCTTGAGCCGCGCTTC 840

Db 781 TACCACTGCTCACTGACAACTTCCCTGCCATTGTCTGCTCTTGAGCCGCGCTTC 840

Oy 841 TGTGCCACAGTGTGGCTCTCCCGGTGACGTGTGAAAGACCCGGTAAATATCAACT 900

Db 841 TGTGCCACAGTGTGGCTCTCCCGGTGACGTGTGAAAGACCCGGTAAATATCAACT 900

Oy 901 CCAGGCCAGATCTCAGCCGCCCTGCACGTATGATAAAGATGATGAGCCACAGAGGCC 960

Db 901 CCAGGCCAGATCTCAGCCGCCCTGCACGTATGATAAAGATGATGAGCCACAGAGGCC 960

Oy 961 ACAGCTTCTACAGAGGATTTACACCTCTCT 991

Db 961 ACAGCTTCTACAGAGGATTTACACCTCTCTCTCT 991

RESULT 12  
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CC The present sequence encodes human uncoupling protein-3s. UCPS can cause  
 CC the reversible uncoupling of electron transport and oxidative  
 CC phosphorylation, which leads to a decrease in the mitochondrial membrane  
 CC potential. This can induce lysis in a tumour cell by inducing the  
 CC expression of MHC class II HLA-DR. These methods can be used for  
 CC regulating cell growth and division to control disease processes by  
 CC manipulating mitochondrial metabolism and the expression of cell surface  
 CC immune proteins. They can be used for treating diseases associated with  
 CC excessive cellular division, aberrant differentiation, and premature  
 CC cellular death, e.g. cancers, autoimmune diseases, neurodegenerative  
 CC disorders etc

XX Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;

Query Match 79.7%; Score 981.4; DB 3; Length 1132;  
 Best Local Similarity 99.4%; Pred. No. 2,7e-233;  
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 TCTGGGATGAGAGCCCTAGAGGCGCTGTGCTGCGCCCTGCGGAGGAGGAGCTCAGAGCC 60  
 1 TCTGGGATGAGAGCCCTAGAGGAGCCCTGTGCTGCGCCCTGCGGAGGAGGAGCTCAGAGCC 60  
 61 CCAAGCGCTGCTGAGAGCCAGGAGGCTGTGAGAGGAGGCTCTCTCTGAGACCTCTCTCG 120  
 61 CCAAGCGCTGCTGAGAGCCAGGAGGCTGTGAGAGGAGGCTCTCTCTGAGACCTCTCTCG 120  
 121 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCTATGAGTGTGAGACTGAGAGCTTCTGAGCTG 180  
 121 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCTATGAGTGTGAGACTGAGAGCTTCTGAGCTG 180  
 181 CCTTCCAGAGTGTGAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 181 CCTTCCAGAGTGTGAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 181 CCTTCCAGAGTGTGAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 241 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 241 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 301 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 301 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 361 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 361 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 421 AGCTTGGGCTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
 421 AGCTTGGGCTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
 481 GGGGCGGAGCAACTCCAGGCTCACTACCCGAGATTTTGGCGGCTGAGCAACAGAGGAGCAT 540  
 481 GGGGCGGAGCAACTCCAGGCTCACTACCCGAGATTTTGGCGGCTGAGCAACAGAGGAGCAT 540  
 541 GGGGCGGAGCAACTCCAGGCTCACTACCCGAGATTTTGGCGGCTGAGCAACAGAGGAGCAT 600  
 541 GGGGCGGAGCAACTCCAGGCTCACTACCCGAGATTTTGGCGGCTGAGCAACAGAGGAGCAT 600  
 601 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 601 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 661 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
 661 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
 721 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 721 GTTACCTTCCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 781 TACCACTGCTCACTGAGCACTTCCCTGAGCACTTTGTCTGTGCTTTGAGAGGCGGCTTC 840  
 781 TACCACTGCTCACTGAGCACTTCCCTGAGCACTTTGTCTGTGCTTTGAGAGGCGGCTTC 840

QY 841 TGTGCGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
 DB 841 TGTGCGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
 QY 901 CCAAGCGCTGCTGAGAGCCAGGAGGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
 DB 901 CCAAGCGCTGCTGAGAGCCAGGAGGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
 QY 961 ACAGCCTTCTACAGGAGATTTACAGCCTCTCT 991  
 DB 961 ACAGCCTTCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 991

RESULT 13

AA14820  
 ID AA14820 standard; cDNA; 1132 BP.

AA14820;  
 13-DEC-2001 (first entry)

Human cDNA encoding partial UCP-3s protein.

Human; Uncoupling protein; UCP-3s; ss; transgenic plant; fuel metabolism;  
 antibacterial; bacterial infection; environmental stress; food.

Homo sapiens.

Key Location/Qualifiers  
 CDS 127..981  
 /tag=a  
 /product="UCP-3s"  
 /partial  
 /note="No start codon"

MO200175131-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US010236.

31-MAR-2000; 2000US-0193533P.

(UYTR-) UNIV TECHNOLOGY CORP.

Berry-Lowe SL, Newell MK;

WPI: 2001-626442/72.

P-PSDB; AAUD9078.

Plants expressing heterologous cell-wall uncoupling protein, have altered

metabolism, resistance to infection and stress sensitivity.

Disclosure; Page 60-61; 72pp; English.

The invention relates to a transgenic plant expressing a cell-wall UCP  
 (uncoupling protein) encoded by a heterologous gene. The heterologous  
 UCP, when expressed in the plant cell wall, plasma membrane or  
 chloroplast regulates the fuel metabolism of the plant. Regulating  
 expression or activity of UCP is used to control fuel metabolism,  
 especially reducing UCP expression produces nutritionally improved plants  
 and protects against infection e.g. bacterial, while decreasing  
 expression improves sensitivity to light and cold. Altering UCP activity  
 can improve crop productivity and durability towards environmental  
 stress, and it eliminates time-consuming and expensive maintenance and  
 repeated application of chemicals. The present sequence encodes human UCP  
 -3s and is used as the heterologous UCP in the method of the invention

Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;

Query Match 79.7%; Score 981.4; DB 5; Length 1132;  
 Best Local Similarity 99.4%; Pred. No. 2,7e-233;





Db 121 CCTTAAAGGAGCTTGGGAGAGGCTTCCAGAGCTATGTTGGAGCTGAAGCTTCAAGAGCTG 180  
 Qy 181 CCTCCACCACTGAGCTGTGAAAGTTCTGTGGGGGAGGAGAGAGGCTGTTTGTCTGAGCTTC 240  
 Db 181 CTTCCACCACTGAGCTGTGAAAGTTCTGTGGGGGAGGAGAGAGGCTGTTTGTCTGAGCTTC 240  
 Qy 241 GTTACTCTTCCATCTGAGAGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTG 300  
 Db 241 GTTACTCTTCCATCTGAGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTG 300  
 Qy 301 GTTCAAGAGGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTG 360  
 Db 301 GTTCAAGAGGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTG 360  
 Qy 361 CGGAGCTGAGGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTG 420  
 Db 361 CGGAGCTGAGGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTG 420  
 Qy 421 AGCTTGGCTCCATCTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTG 480  
 Db 421 AGCTTGGCTCCATCTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTG 480  
 Qy 481 GGCGGAGGAGCACTCCAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAG 540  
 Db 481 GGCGGAGGAGCACTCCAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAG 540  
 Qy 541 GGGGTGAGCTGTGAGGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAG 600  
 Db 541 GGGGTGAGCTGTGAGGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAG 600  
 Qy 601 GTTGGGAGGAGCACTCCAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAG 660  
 Db 601 GTTGGGAGGAGCACTCCAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAG 660  
 Qy 661 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
 Db 661 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720  
 Qy 721 GCTATGCTCACTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 Db 721 GCTATGCTCACTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 Qy 781 TACCACTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 840  
 Db 781 TACCACTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 840  
 Qy 841 TGTGCACTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 900  
 Db 841 TGTGCACTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 900  
 Qy 901 CCAGGCACTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 960  
 Db 901 CCAGGCACTGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 960  
 Qy 961 ACAAGCTTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 991  
 Db 961 ACAAGCTTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 991

RESULT 15

ABQ73000 standard, cDNA, 1132 BP.

ABQ73000;

20-SEP-2002 (first entry)

UCP3S cDNA clone nucleotide sequence.

UCPI3, UCP3S; diabetes; obesity; diabetic related condition; GKR; gene therapy; anti-diabetic; anorectic; cardiomy; nephroretic; GK; antilipemic; blood glucose; glucokinase regulatory protein; liver;

KW glucokinase; hepatic triglyceride accumulation; fibrinogen; HDL; KW hepatic fatty acid oxidation; high density lipoprotein; cholesterol; KW glucose; gestational diabetes; hyperglycemic related disorder; KW kidney related disorder; cardiovascular disorder; gene; se. OS Unidentified.

Key	Location/Qualifiers
FT CDS	154..981
FT	/*tag= a
FT	/product= "UCP3S protein"
US	US2002065239-A1.
PD	30-MAY-2002.
XX	14-MAR-2001; 2001US-00808457.
XX	15-MAR-2000; 2000US-0266328P.
XX	(CAPL/) CAPLAN S L.
XX	(BOET/) BOETTCHER B R.
XX	(SLOS/) SLOSBURG E D.
XX	(CONN/) CONNELLY S.
XX	(KALE/) KALEKO M.
XX	(DESA/) DESAI U J.
XX	Caplan SL, Boettcher BR, Sloberg ED, Connelly S, Kaleko M, Desai UJ, P-PSDB; ABB81611.
XX	WPI: 2002-556735/59.
XX	P-PSDB; ABB81611.
XX	Treating condition related to elevated blood glucose levels, especially diabetes or obesity, involves administering polynucleotide sequence encoding glucokinase regulatory protein, to a subject.
XX	Disclosure; Page 17-18; 42pp; English.
XX	The present invention describes a method (M1) for treating a condition related to elevated blood glucose levels, which involves administering a polynucleotide sequence encoding a glucokinase regulatory protein (GKR) to a subject. Also described: (1) increasing liver glucokinase (GK) activity, by administering a polynucleotide sequence encoding GKR; and (2) a method (M2) treating diabetes or diabetes-related condition, by administering to a subject, one or more metabolism modifying proteins and peptides in combination with GK or GKR, or their combination. (M1) and (M2) can be used for treating diabetes (type I and II diabetes) or diabetes-related conditions such as obesity, increased hepatic triglyceride accumulation, reduced hepatic fatty acid oxidation, increased fibrinogen levels, decreased apo A-I levels, decreased high density lipoprotein (HDL) cholesterol levels and decreased hepatic glucose utilization. The methods are also useful for treating gestational diabetes, hyperglycemic related disorders such as increased cholesterol, kidney related disorders and cardiovascular disorders. The methods overcome a limitation to the over-expression of GK in the liver which usually increases liver size and hepatic fat accumulation in normal and diabetic mice. The present sequence encodes a UCP3S protein which is given in the exemplification of the present invention
XX	Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;
XX	Query Match 79.7%; Score 981.4; DB 6; Length 1132;
XX	Best Local Similarity 99.4%; Pred. No. 2.7e-233;
XX	Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy	1 TCTGGAGTGAAGCCCTAGAGAGCCCTGTGCTGCGCCCTGAGAGAGTCAAGCC 60
Db	1 TCTGGAGTGAAGCCCTAGAGAGCCCTGTGCTGCGCCCTGAGAGAGTCAAGCC 60
Qy	61 CCACGCTGCACTGAAGCCCAAGGCTGTGAGAGAGGCTTCTCTTGAAGCTTCTCTCGG 120
Db	61 CCACGCTGCACTGAAGCCCAAGGCTGTGAGAGAGGCTTCTCTTGAAGCTTCTCTCGG 120

QY 121 CCTAAGGGAATGAGGAGGAGGCTTCAAGACTATGTTGACTGAGGCTTCAAGCGTG 180  
DB 121 CCTAAGGGAATGAGGAGGAGGCTTCAAGACTATGTTGACTGAGGCTTCAAGCGTG 180  
QY 181 CCTCCACCAATGAGCTGTGAAGTTCTTGGGGGAGGAGCAAGAGGCTTGTCTGACCTC 240  
DB 181 CCTCCACCAATGAGCTGTGAAGTTCTTGGGGGAGGAGCAAGAGGCTTGTCTGACCTC 240  
QY 241 GTTACCTTTCACATGAGCAAGGCAAGGCTTCAAGATCCAGGGGAGAACCAAGGCG 300  
DB 241 GTTACCTTTCACATGAGCAAGGCTTCAAGATCCAGGGGAGAACCAAGGCG 300  
QY 301 GTCCAGAGGAGGCTGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 360  
DB 301 GTCCAGAGGAGGCTGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 360  
QY 361 CGGACTGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 420  
DB 361 CGGACTGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 420  
QY 421 AGCTTGGCTTCATCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 480  
DB 421 AGCTTGGCTTCATCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 480  
QY 481 GGGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 540  
DB 481 GGGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 540  
QY 541 GGGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 600  
DB 541 GGGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 600  
QY 601 CTGAGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 660  
DB 601 CTGAGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 660  
QY 661 GCGAGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 720  
DB 661 GCGAGGAGGAGGAGTCCCTGAGGAGGCTTCAAGTGGCTGAGGAGGCTTCAAGTGGCTG 720  
QY 721 GCTATGTCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 780  
DB 721 GCTATGTCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 780  
QY 781 TACCACTGTCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 840  
DB 781 TACCACTGTCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 840  
QY 841 TGTGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 900  
DB 841 TGTGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 900  
QY 901 CCAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 960  
DB 901 CCAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 960  
QY 961 ACAAGCTTTCATCAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 991  
DB 961 ACAAGCTTTCATCAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 991

Search completed: May 18, 2004, 12:31:25  
Job time : 532 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: May 17, 2004, 11:50:46 ; Search time 23 Seconds  
(without alignments)  
700.318 Million cell updates/sec

Title: US-09-423-410-4  
Perfect score: 1620  
Sequence: 1 MVLGKPSDVPPTMAVFLGA.....TYEQLKRAIMKVMLESPF 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
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2: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*  
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6: /cgn2\_6/prodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	100.0	312	3	US-09-142-565-2 Sequence 2, Appl1
2	1620	100.0	312	4	US-09-808-457-2 Sequence 2, Appl1
3	1620	100.0	312	4	US-09-423-410-4 Sequence 4, Appl1
4	1599	98.7	310	4	US-09-743-847-5 Sequence 5, Appl1
5	1430	88.3	275	4	US-09-808-457-4 Sequence 4, Appl1
6	1430	88.3	275	4	US-09-423-410-6 Sequence 6, Appl1
7	1369	84.5	308	2	US-08-937-466-2 Sequence 2, Appl1
8	1369	84.5	308	2	US-09-172-528-2 Sequence 2, Appl1
9	1369	84.5	308	3	US-09-318-199-2 Sequence 2, Appl1
10	1369	84.5	308	3	US-09-503-579-2 Sequence 2, Appl1
11	1341	82.8	432	2	US-08-937-466-4 Sequence 4, Appl1
12	1341	82.8	432	2	US-09-172-528-4 Sequence 4, Appl1
13	1341	82.8	432	3	US-09-318-199-4 Sequence 4, Appl1
14	1341	82.8	432	3	US-09-503-579-4 Sequence 4, Appl1
15	1152.5	71.1	309	4	US-10-001-0518-2 Sequence 2, Appl1
16	1149.5	71.0	309	4	US-09-743-847-4 Sequence 4, Appl1
17	1147.5	70.8	309	1	US-08-518-8788-51 Sequence 51, Appl1
18	1147.5	70.8	309	2	US-08-807-8618-51 Sequence 51, Appl1
19	1147.5	70.8	309	2	US-08-470-868A-51 Sequence 51, Appl1
20	1147.5	70.8	309	3	US-09-210-681-51 Sequence 51, Appl1
21	1147.5	70.8	309	3	US-08-946-719A-51 Sequence 51, Appl1
22	1147.5	70.8	309	4	US-09-547-983-51 Sequence 51, Appl1
23	1110.5	68.5	299	2	US-08-518-8788-56 Sequence 56, Appl1
24	1110.5	68.5	299	2	US-08-470-868A-56 Sequence 56, Appl1
25	1098	67.8	256	2	US-08-937-466-6 Sequence 6, Appl1
26	1098	67.8	256	2	US-09-172-528-6 Sequence 6, Appl1
27	1098	67.8	256	3	US-09-318-199-6 Sequence 6, Appl1

28	1098	67.8	256	3	US-09-503-579-6 Sequence 6, Appl1
29	1012.5	62.5	303	1	US-08-294-522B-36 Sequence 36, Appl1
30	1009.5	62.3	303	1	US-08-518-878B-37 Sequence 37, Appl1
31	1009.5	62.3	303	2	US-08-807-861A-37 Sequence 37, Appl1
32	1009.5	62.3	303	2	US-08-470-868A-37 Sequence 37, Appl1
33	1009.5	62.3	303	3	US-09-210-681-37 Sequence 37, Appl1
34	1009.5	62.3	303	3	US-08-946-719A-37 Sequence 37, Appl1
35	1009.5	62.3	303	4	US-09-547-983-37 Sequence 37, Appl1
36	910.5	56.2	307	4	US-09-743-847-3 Sequence 37, Appl1
37	889.5	54.9	307	2	US-08-807-861A-56 Sequence 56, Appl1
38	889.5	54.9	307	3	US-09-210-681-56 Sequence 56, Appl1
39	889.5	54.9	307	3	US-08-946-719A-56 Sequence 56, Appl1
40	889.5	54.9	307	4	US-09-547-983-56 Sequence 56, Appl1
41	887	54.8	306	5	PCT-US94-09799-1 Sequence 1, Appl1
42	512	31.6	290	4	US-09-743-847-2 Sequence 118, Appl1
43	512	31.6	291	4	US-09-482-273-118 Sequence 2, Appl1
44	509.5	31.5	291	4	US-09-501-558-2 Sequence 2, Appl1
45	485	29.9	95	3	US-09-142-565-6 Sequence 6, Appl1

## ALIGNMENTS

RESULT 1  
US-09-142-565-2  
Sequence 2, Application US/09142565A

Patent No. 6187560  
GENERAL INFORMATION:

APPLICANT: Lee James Beeley  
APPLICANT: Kelly Paine

TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GH-30002

CURRENT APPLICATION NUMBER: US/09/142,565A  
CURRENT FILING DATE: 1999-06-30

EARLIER APPLICATION NUMBER: 9704551.2  
EARLIER FILING DATE: 1997-03-05

EARLIER APPLICATION NUMBER: 9705614.7  
EARLIER FILING DATE: 1997-03-18

EARLIER APPLICATION NUMBER: 97305305.1  
EARLIER FILING DATE: 1997-07-16

NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2  
LENGTH: 312

TYPE: PRT  
ORGANISM: HOMO SAPIEN

US-09-142-565-2

Query Match 100.0%; Score 1620; DB 3; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.1e-179;

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVLGKPSDVPPTMAVFLGAGTACPADLVTFPLDTRAKVRLQIGENQAVQTRALVQYRG	60
DB	1	MVLGKPSDVPPTMAVFLGAGTACPADLVTFPLDTRAKVRLQIGENQAVQTRALVQYRG	60
QY	61	VLTGTTLMVTBGPSPYNGVLVAGLORQMSFASIRIGLVSVQVYTPKQDSSLTTRI	120
DB	61	VLTGTTLMVTBGPSPYNGVLVAGLORQMSFASIRIGLVSVQVYTPKQDSSLTTRI	120
QY	121	IAGCTGAMAVTCAOPTDVVKVRFQASIHGSPSRDKEYSGTMDAVYTIAREEGVRLMK	180
DB	121	IAGCTGAMAVTCAOPTDVVKVRFQASIHGSPSRDKEYSGTMDAVYTIAREEGVRLMK	180
QY	181	GLTLENIRNAIVNCAEVYVDILKELLDYHLTDNPFCHFVSAFGAGFCATTVASPVVD	240
DB	181	GLTLENIRNAIVNCAEVYVDILKELLDYHLTDNPFCHFVSAFGAGFCATTVASPVVD	240
QY	241	VKTRVNSPBGQYFSPIDCMIKVVAOEGPTAFYKGFPSFLRIGSNVWVFPVTEOLKRA	300
DB	241	VKTRVNSPBGQYFSPIDCMIKVVAOEGPTAFYKGFPSFLRIGSNVWVFPVTEOLKRA	300

QY 301 LMKVQMLRESPP 312  
Db 301 LMKVQMLRESPP 312

## RESULT 2

US-09-808-457-2  
Sequence 2, Application US/09808457  
Patent No. 6608038  
GENERAL INFORMATION:  
APPLICANT: Boetcher, Brian  
APPLICANT: Caplan, Shari  
APPLICANT: Kalejo, Michael  
APPLICANT: Connolly, Sheila  
APPLICANT: Desai, Urv  
APPLICANT: Slobberg, Eric  
TITLE OF INVENTION: Methods and Compositions For Treatment  
of Diabetes and Related Conditions Via Gene Therapy  
FILE REFERENCE: 4-31353A/USN  
CURRENT APPLICATION NUMBER: US/09/808,457  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/xxx,xxx  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Protein UCP3L  
US-09-808-457-2

Query Match 100.0%; Score 1620; DB 4; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.1e-179;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVOTARLVQYRG 60  
Db 1 MGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVOTARLVQYRG 60  
QY 61 VLGITLTVWRTGEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSLTTRI 120  
Db 61 VLGITLTVWRTGEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSLTTRI 120  
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSRDKTSGTMDAYRTTAREEGVGLMK 180  
Db 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSRDKTSGTMDAYRTTAREEGVGLMK 180  
QY 181 GTLPNIMRNAIYNCAEVYTDILKEKLDYHLITDNPFCHPVSAGAGCATVVASPDVY 240  
Db 181 GTLPNIMRNAIYNCAEVYTDILKEKLDYHLITDNPFCHPVSAGAGCATVVASPDVY 240  
QY 241 VKTRVNSPPGQYFSPFLDCMIRVVAQEGPTAFYKGFPSFLRGSNNVMFTYEQLEKRA 300  
Db 241 VKTRVNSPPGQYFSPFLDCMIRVVAQEGPTAFYKGFPSFLRGSNNVMFTYEQLEKRA 300  
QY 301 LMKVQMLRESPP 312  
Db 301 LMKVQMLRESPP 312

## RESULT 3

US-09-423-410-4  
Sequence 4, Application US/09423410  
Patent No. 6620594  
GENERAL INFORMATION:  
APPLICANT: Giacobino, Jean-Paul  
APPLICANT: Muzzin, Patrick  
APPLICANT: Boss, Olivier  
TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3  
FILE REFERENCE: 4-30353/A  
CURRENT APPLICATION NUMBER: US/09/423,410

CURRENT FILING DATE: 1999-11-04  
EARLIER APPLICATION NUMBER: PCT/EP98/02645  
EARLIER FILING DATE: 1998-05-05  
EARLIER APPLICATION NUMBER: 1072/97  
EARLIER FILING DATE: 1997-05-07  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4

US-09-423-410-4  
Sequence 4, Application US/09423410  
Patent No. 6620594  
GENERAL INFORMATION:  
APPLICANT: Boetcher, Brian  
APPLICANT: Caplan, Shari  
APPLICANT: Kalejo, Michael  
APPLICANT: Connolly, Sheila  
APPLICANT: Desai, Urv  
APPLICANT: Slobberg, Eric  
TITLE OF INVENTION: Methods and Compositions For Treatment  
of Diabetes and Related Conditions Via Gene Therapy  
FILE REFERENCE: 4-31353A/USN  
CURRENT APPLICATION NUMBER: US/09/808,457  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/xxx,xxx  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Protein UCP3L  
US-09-423-410-4

Query Match 100.0%; Score 1620; DB 4; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.1e-179;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVOTARLVQYRG 60  
Db 1 MGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVOTARLVQYRG 60  
QY 61 VLGITLTVWRTGEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSLTTRI 120  
Db 61 VLGITLTVWRTGEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSLTTRI 120  
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSRDKTSGTMDAYRTTAREEGVGLMK 180  
Db 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSRDKTSGTMDAYRTTAREEGVGLMK 180  
QY 181 GTLPNIMRNAIYNCAEVYTDILKEKLDYHLITDNPFCHPVSAGAGCATVVASPDVY 240  
Db 181 GTLPNIMRNAIYNCAEVYTDILKEKLDYHLITDNPFCHPVSAGAGCATVVASPDVY 240  
QY 241 VKTRVNSPPGQYFSPFLDCMIRVVAQEGPTAFYKGFPSFLRGSNNVMFTYEQLEKRA 300  
Db 241 VKTRVNSPPGQYFSPFLDCMIRVVAQEGPTAFYKGFPSFLRGSNNVMFTYEQLEKRA 300  
QY 301 LMKVQMLRESPP 312  
Db 301 LMKVQMLRESPP 312

## RESULT 4

US-09-743-847-5  
Sequence 5, Application US/09743847  
Patent No. 6602694  
GENERAL INFORMATION:  
APPLICANT: Amvlin Pharmaceuticals, Inc.  
APPLICANT: Albrandt, Keith  
APPLICANT: Beaumont, Kevin  
APPLICANT: Young, Andrew  
TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE  
FILE REFERENCE: 235/108,0026  
CURRENT APPLICATION NUMBER: US/09/743,847  
CURRENT FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: US 60/092,737  
PRIOR FILING DATE: 1998-07-14  
PRIOR APPLICATION NUMBER: PCT/US99/15861  
PRIOR FILING DATE: 1999-07-14  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-743-847-5

Query Match 98.7%; Score 1599; DB 4; Length 310;  
Best Local Similarity 99.4%; Pred. No. 3.1e-177;  
Matches 310; Conservative 0; Mismatches 0; Indels 2; Gaps 1;





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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-466-2
```

Query Match 84.5%; Score 1369; DB 2; Length 308;

Best Local Similarity 85.3%; Pred. No. 1.7e-150; Mismatches 24; Indels 4; Gaps 2;

Matches 266; Conservative 18; Mismatches 24; Indels 4; Gaps 2;

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QY 1 MVLGKPSDVPPTMAVKFLGAGTAACPADLVTPPLDTAKVRLIOIGENQAVQTARLVQYRG 60
DB 1 MVLGKPSDVPPTMAVKFLGAGTAACPADLVTPPLDTAKVRLIOIGENQAVQTARLVQYRG 57
QY 61 VGTITLMTWRTGSPSPVNGVAGLQROMSFASIRIGLVDSVKQYTPPGADNSLTTTRI 120
DB 58 VGTITLMTWRTGSPSPVNGVAGLQROMSFASIRIGLVDSVKQYTPPGADNSLTTTRI 117
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 180
DB 118 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 176
QY 181 GTLPNIRNAIVNCAEVVTDILKEKLDYHLITDNFPCHFVAFGAGCATVVASPVVY 240
DB 177 GTLPNIRNAIVNCAEVVTDILKEKLDYHLITDNFPCHFVAFGAGCATVVASPVVY 236
QY 241 VTRVYNSPPGQFSPDLDMIKVAOEGPTAFYKGFPSFLRIGSNVNMVFYTYEQLKRA 300
DB 237 VTRVYNSPPGQFSPDLDMIKVAOEGPTAFYKGFPSFLRIGSNVNMVFYTYEQLKRA 296
QY 301 LMKVQMLRESPPF 312
DB 297 LMKVQMLRESPPF 308
```

## RESULT 8

US-09-172-528-2

Sequence 2, Application US/09172528

Patent No. 5952469

GENERAL INFORMATION:

APPLICANT: Zhang, Ning

APPLICANT: Amarel, M. Catherine

APPLICANT: Chen, Jin-Long

TITLE OF INVENTION: UCP3 Genes

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-172-528-2
```

Query Match 84.5%; Score 1369; DB 2; Length 308;

Best Local Similarity 85.3%; Pred. No. 1.7e-150; Mismatches 24; Indels 4; Gaps 2;

Matches 266; Conservative 18; Mismatches 24; Indels 4; Gaps 2;

```
QY 1 MVLGKPSDVPPTMAVKFLGAGTAACPADLVTPPLDTAKVRLIOIGENQAVQTARLVQYRG 60
DB 1 MVLGKPSDVPPTMAVKFLGAGTAACPADLVTPPLDTAKVRLIOIGENQAVQTARLVQYRG 57
QY 61 VGTITLMTWRTGSPSPVNGVAGLQROMSFASIRIGLVDSVKQYTPPGADNSLTTTRI 120
DB 58 VGTITLMTWRTGSPSPVNGVAGLQROMSFASIRIGLVDSVKQYTPPGADNSLTTTRI 117
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 180
DB 118 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 176
QY 181 GTLPNIRNAIVNCAEVVTDILKEKLDYHLITDNFPCHFVAFGAGCATVVASPVVY 240
DB 177 GTLPNIRNAIVNCAEVVTDILKEKLDYHLITDNFPCHFVAFGAGCATVVASPVVY 236
QY 241 VTRVYNSPPGQFSPDLDMIKVAOEGPTAFYKGFPSFLRIGSNVNMVFYTYEQLKRA 300
DB 237 VTRVYNSPPGQFSPDLDMIKVAOEGPTAFYKGFPSFLRIGSNVNMVFYTYEQLKRA 296
QY 301 LMKVQMLRESPPF 312
DB 297 LMKVQMLRESPPF 308
```

## RESULT 9

US-09-318-199-2

Sequence 2, Application US/09318199

Patent No. 6025469

GENERAL INFORMATION:

APPLICANT: Zhang, Ning

APPLICANT: Amarel, M. Catherine

APPLICANT: Chen, Jin-Long

TITLE OF INVENTION: UCP3 Genes

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk



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      ZIP: 94010
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/937,466
      FILING DATE:
      CLASSIFICATION: 435
      ATTORNEY/AGENT INFORMATION:
      NAME: OSMAN, RICHARD A
      REGISTRATION NUMBER: 36,627
      REFERENCE/DOCKET NUMBER: T97-009
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (650) 343-4341
      TELEFAX: (650) 343-4342
      INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 432 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      US-08-937-466-4

```

```

Query Match      82.8%; Score 1341; DB 2; Length 432;
Best Local Similarity 85.6%; Pred. No. 5.1e-147;
Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

```

```

QY      1 MVLGKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKRLQIOGENOVAQTARLVQYRG 60
DB      1 MVLGQPSVPTTVPYVKFLGAGTAACFADLVTFPLDTAKRLQIOGENOVAQTARLVQYRG 57
QY      61 VLGLTLVWRTGEGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYTTKGDNSLTTRI 120
DB      58 VLGLTLVWRTGEGSPYSGVLVAGLHROMSPASIRIGLYDSVKQYTFPGADHSSVALRI 117
QY      121 LAGCTGMAVTCACOPTDVVVRFOASIHLPSSDRKSGTMDAYRTIAREEGVRLMK 180
DB      118 LAGCTGMAVTCACOPTDVVVRFOAMIRLG-TGGERKTRGTMDAYRTIAREEGVRLMK 176
QY      177 GTWPNITRNALVNCHEMTYDIIKEKLESHLFTDNFCHFSVAGAGFCATVVASPDV 240
DB      181 GTLPINIMENALVNCHEMTYDIIKEKLESHLFTDNFCHFSVAGAGFCATVVASPDV 236
QY      241 VETRYMNSPPQYSPPLDCMIRVAOEGPTAFYKGFSTPSFLRLGSMNTVMFTYEQLKRA 300
DB      237 VETRYMNAAPLGRYSPLHCLMKVVAOEGPTAFYKGFVPSFLRLGSMNTVMFTYEQLKRA 296
QY      301 LMKVQ 305
DB      297 LMKVQ 301

```

RESULT 12  
US-09-172-528-4  
Sequence 4, Application US/09172528  
Patent No. 5952469

GENERAL INFORMATION:  
APPLICANT: Zhang, Ning  
APPLICANT: Amaral, M. Catherine  
APPLICANT: Chen, Jin-Long  
TITLE OF INVENTION: UCP3 Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:

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      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/172,528
      FILING DATE:
      CLASSIFICATION:
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/937,466
      FILING DATE:
      ATTORNEY/AGENT INFORMATION:
      NAME: OSMAN, RICHARD A
      REGISTRATION NUMBER: 36,627
      REFERENCE/DOCKET NUMBER: T97-009
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (650) 343-4341
      TELEFAX: (650) 343-4342
      INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 432 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      US-09-172-528-4

```

```

Query Match      82.8%; Score 1341; DB 2; Length 432;
Best Local Similarity 85.6%; Pred. No. 5.1e-147;
Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

```

```

QY      1 MVLGKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKRLQIOGENOVAQTARLVQYRG 60
DB      1 MVLGQPSVPTTVPYVKFLGAGTAACFADLVTFPLDTAKRLQIOGENOVAQTARLVQYRG 57
QY      61 VLGLTLVWRTGEGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYTTKGDNSLTTRI 120
DB      58 VLGLTLVWRTGEGSPYSGVLVAGLHROMSPASIRIGLYDSVKQYTFPGADHSSVALRI 117
QY      121 LAGCTGMAVTCACOPTDVVVRFOASIHLPSSDRKSGTMDAYRTIAREEGVRLMK 180
DB      118 LAGCTGMAVTCACOPTDVVVRFOAMIRLG-TGGERKTRGTMDAYRTIAREEGVRLMK 176
QY      177 GTWPNITRNALVNCHEMTYDIIKEKLESHLFTDNFCHFSVAGAGFCATVVASPDV 240
DB      181 GTLPINIMENALVNCHEMTYDIIKEKLESHLFTDNFCHFSVAGAGFCATVVASPDV 236
QY      241 VETRYMNSPPQYSPPLDCMIRVAOEGPTAFYKGFSTPSFLRLGSMNTVMFTYEQLKRA 300
DB      237 VETRYMNAAPLGRYSPLHCLMKVVAOEGPTAFYKGFVPSFLRLGSMNTVMFTYEQLKRA 296
QY      301 LMKVQ 305
DB      297 LMKVQ 301

```

RESULT 13  
US-09-318-199-4  
Sequence 4, Application US/09318199  
Patent No. 6023469

GENERAL INFORMATION:  
APPLICANT: Zhang, Ning  
APPLICANT: Amaral, M. Catherine  
APPLICANT: Chen, Jin-Long  
TITLE OF INVENTION: UCP3 Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/318,199  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/937,466  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-318-199-4

Query Match 82.8%; Score 1341; DB 3; Length 432;  
Best Local Similarity 85.6%; Pred. No. 5,1e-147;  
Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 1 MVLKPSDVEPTMAVFLGAGTACFADLVTFPLDTAKVRLQIGENQAVQTARLYOYRG 60  
DB 1 MVLGQSEVPPTTVVFLGAGTACFADLVTFPLDTAKVRLQIGENQAVQTARLYOYRG 57  
QY 61 VLGTITLMTWTEPCSPYNGVLVAGLORQMSFASIRIGLYDSVQVTPKADNSSLTTRI 120  
DB 58 VLGTITLMTWTEPCSPYSGVLVAGLHROMSFASIRIGLYDSVQVTPKADNSSLTTRI 117  
QY 121 LAGCTGAMAVTCAOPTDVVKVRFQASIHLPSSDRKSGTMDAVYTIAREEGVRLMK 180  
DB 118 LAGCTGAMAVTCAOPTDVVKVRFQAMIRLG-TGGERKYGTDYVYTIAREEGVRLMK 176  
QY 181 GLTLENIRNAIVNCAEVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDV 240  
DB 177 GTWPNITRNAIVNCAEVYTDILKEKLBESHLFTDNPFCHVSAFGAGFCATVVASPDV 236  
QY 241 VKTRYNMSPGQYFSPDLCMKVVAOEGPTAFYKGFPSFLRIGSNVVMFVTEQLKRA 300  
DB 237 VKTRYNMSPGQYFSPDLCMKVVAOEGPTAFYKGFVPSFLRIGAMVVMFVTEQLKRA 296  
QY 301 LMKVQ 305  
DB 297 LMKVQ 301

RESULT 14  
US-09-503-579-4  
Sequence 4, Application US/09503579  
Patent No. 6248561  
GENERAL INFORMATION:  
APPLICANT: Zhang, Ning  
APPLICANT: Amaral, M. Catherine  
APPLICANT: Chen, Jin-long  
TITLE OF INVENTION: UCP3 Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY IAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA

ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/503,579  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,466  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-503-579-4

Query Match 82.8%; Score 1341; DB 3; Length 432;  
Best Local Similarity 85.6%; Pred. No. 5,1e-147;  
Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 1 MVLKPSDVEPTMAVFLGAGTACFADLVTFPLDTAKVRLQIGENQAVQTARLYOYRG 60  
DB 1 MVLGQSEVPPTTVVFLGAGTACFADLVTFPLDTAKVRLQIGENQAVQTARLYOYRG 57  
QY 61 VLGTITLMTWTEPCSPYNGVLVAGLORQMSFASIRIGLYDSVQVTPKADNSSLTTRI 120  
DB 58 VLGTITLMTWTEPCSPYSGVLVAGLHROMSFASIRIGLYDSVQVTPKADNSSLTTRI 117  
QY 121 LAGCTGAMAVTCAOPTDVVKVRFQASIHLPSSDRKSGTMDAVYTIAREEGVRLMK 180  
DB 118 LAGCTGAMAVTCAOPTDVVKVRFQAMIRLG-TGGERKYGTDYVYTIAREEGVRLMK 176  
QY 181 GLTLENIRNAIVNCAEVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDV 240  
DB 177 GTWPNITRNAIVNCAEVYTDILKEKLBESHLFTDNPFCHVSAFGAGFCATVVASPDV 236  
QY 241 VKTRYNMSPGQYFSPDLCMKVVAOEGPTAFYKGFPSFLRIGSNVVMFVTEQLKRA 300  
DB 237 VKTRYNMSPGQYFSPDLCMKVVAOEGPTAFYKGFVPSFLRIGAMVVMFVTEQLKRA 296  
QY 301 LMKVQ 305  
DB 297 LMKVQ 301

RESULT 15  
US-10-001-051B-2  
Sequence 2, Application US/10001051B  
Patent No. 6670138  
GENERAL INFORMATION:  
APPLICANT: Gonzalez-Zulueta, Mirella  
APPLICANT: Shamloo, Mehrdad  
APPLICANT: McFarland, K.C.  
APPLICANT: Chin, Daniel  
APPLICANT: Mieloch, Tadeusz  
APPLICANT: Welcher, Thorsten  
APPLICANT: AGY Therapeutics, Inc.  
TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING  
TITLE OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES  
FILE REFERENCE: 019488-003010US

;; CURRENT APPLICATION NUMBER: US/10/001,051B  
;; CURRENT FILING DATE: 2002-06-25  
;; PRIOR APPLICATION NUMBER: US 60/244,946  
;; PRIOR FILING DATE: 2000-11-01  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 2  
;; LENGTH: 309  
;; TYPE: PR1  
;; ORGANISM: Unknown Organism  
;; FEATURE:  
;; OTHER INFORMATION: Description of Unknown Organism: Any animal  
;; OTHER INFORMATION: source, typically mammalian, most typically human  
US-10-001-051B-2

Query Match 71.1%; Score 1152.5; DB 4; Length 309;  
Best Local Similarity 72.2%; Pred. No. 2.5e-125;  
Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;

QY 1 MWGLKPSDVPPTMAVKFLGAGTACFADLVTFPLDTAKVRLQIQENQA-VQTAFLVQYR 59  
DB 1 MWGFKATDVPPTATVKFLGAGTACFADLVTFPLDTAKVRLQIQENQA-VQTAFLVQYR 60  
QY 60 GVLGTTILMTVRTEGRCSPYNGLVAGIQRMSPASTRIGLYDSVKQVYTFKGDNSLTTR 119  
DB 61 GVMGTTILMTVRTEGRCSPYNGLVAGIQRMSPASTRIGLYDSVKQVYTFKGDNSLTTR 119  
QY 120 ILAGCTGMAVTCAGPTDVVVRFOASIHLPSSRSRDKYSGTMDAYRTIAREEGVRCIM 179  
DB 120 ILAGCTGMAVTCAGPTDVVVRFOASIHLPSSRSRDKYSGTMDAYRTIAREEGVRCIM 176  
QY 180 KGTLPNIMNNAIVNCAEVVYDILKEKLDYHLITDNPCHVSAFAGFCATVVASPYD 239  
DB 177 KGTSPVARNALIVNCAELVYDILKEKLDYHLITDNPCHVSAFAGFCATVVASPYD 236  
QY 240 VKTRVYVNSPFGQYPSBLDCMTKMTVAQEGPTAFYKGFSPFLRIGSNVVMFVYEQLR 299  
DB 237 VKTRVYVNSPFGQYPSBLDCMTKMTVAQEGPTAFYKGFSPFLRIGSNVVMFVYEQLR 296  
QY 300 ALMKVQMLRESPPF 312  
DB 297 ALMAACTSREAPF 309

Search completed: May 17, 2004, 11:54:30  
Job time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comphen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:53:27 ; Search time 48 seconds  
(without alignments)  
1808.699 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620  
Sequence: 1 MVGLKPSDVPPTMAVKFLGA.....TYEQLKRLMKYQMLRESPP 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/2/pubppaa/PCF\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1620	100.0	312	9	US-09-734-134-2
2	1620	100.0	312	9	US-09-826-507-2
3	1620	100.0	312	9	US-09-808-457-2
4	1620	100.0	312	12	US-10-671-628-9
5	1556	96.0	325	14	US-10-270-861-35
6	1430	86.3	275	9	US-09-808-457-4
7	1430	86.3	284	10	US-09-823-886A-6
8	1152.5	71.1	309	9	US-09-884-814-8
9	1152.5	71.1	309	13	US-10-001-051B-2
10	1152.5	71.1	309	15	US-10-197-019-3
11	1149.5	71.0	309	9	US-09-884-814-1
12	1149.5	71.0	309	12	US-10-336-472-132
13	1149.5	71.0	309	12	US-10-671-628-8
14	1149.5	71.0	309	14	US-10-270-861-34
15	1149.5	71.0	309	14	US-10-265-689-1

16	1149.5	71.0	314	10	US-09-823-886A-4	Sequence 4, Appli
17	1147.5	70.8	309	9	US-09-884-814-6	Sequence 6, Appli
18	1142.5	70.5	321	12	US-10-336-472-130	Sequence 110, App
19	919	56.7	306	12	US-10-037-417-89	Sequence 89, Appl
20	910.5	56.2	307	10	US-09-823-886A-2	Sequence 27, Appli
21	910.5	56.2	307	12	US-10-037-417-87	Sequence 87, Appli
22	905	55.9	306	12	US-10-037-417-90	Sequence 88, Appli
23	902.5	55.7	307	12	US-10-037-417-88	Sequence 7, Appli
24	902.5	55.7	307	12	US-10-671-628-7	Sequence 33, Appli
25	902.5	55.7	307	14	US-10-270-861-33	Sequence 91, Appl
26	873.5	53.9	307	12	US-10-037-417-91	Sequence 26, Appli
27	736.5	45.5	271	12	US-10-037-417-26	Sequence 5, Appli
28	687	42.4	306	12	US-10-671-628-5	Sequence 63117, A
29	681.5	42.1	345	12	US-10-425-114-65317	Sequence 237696,
30	676	41.7	305	12	US-10-424-599-237696	Sequence 2, Appli
31	675.5	41.7	303	12	US-10-671-628-2	Sequence 4, Appli
32	651	40.2	314	12	US-10-671-628-6	Sequence 6, Appli
33	592	36.5	268	12	US-10-671-628-4	Sequence 11, Appl
34	521	32.2	322	14	US-10-270-861-11	Sequence 13, Appl
35	521	32.2	325	14	US-10-270-861-13	Sequence 7, Appli
36	512	31.6	322	14	US-10-270-861-7	Sequence 118, App
37	512	31.6	325	14	US-10-270-861-1	Sequence 152, App
38	512	31.6	335	10	US-09-984-271-118	Sequence 2476, Ap
39	512	31.6	335	12	US-10-262-511-152	Sequence 276094,
40	509	31.4	325	12	US-10-108-260A-2476	Sequence 276095,
41	500.5	30.9	291	15	US-10-424-599-276094	Sequence 52234, A
42	496.5	30.6	317	12	US-10-424-599-276095	Sequence 9, Appli
43	487.5	30.1	341	12	US-10-425-114-52234	
44	487.5	30.1	341	12	US-10-270-861-9	
45	486.5	30.0	353	14	US-10-270-861-9	

## ALIGNMENTS

RESULT 1  
US-09-734-134-2  
Sequence 2, Application US/09734134  
Patent No. US20010010929A1  
GENERAL INFORMATION:  
APPLICANT: Lee James Beeley  
APPLICANT: Kelly Payne  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GH-10002-D1  
CURRENT APPLICATION NUMBER: US/09/734,134  
CURRENT FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: GB 9704551.2  
PRIOR FILING DATE: 1997-03-05  
PRIOR APPLICATION NUMBER: GB 9705614.7  
PRIOR FILING DATE: 1997-03-18  
PRIOR APPLICATION NUMBER: EP 97305305.1  
PRIOR FILING DATE: 1997-07-16  
PRIOR APPLICATION NUMBER: GB 9800633  
PRIOR FILING DATE: 1998-03-02  
PRIOR APPLICATION NUMBER: 09/142,565  
PRIOR FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 312  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-09-734-134-2

Query Match 100.0%; Score 1620; DB 9; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.2e-167;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MVGLKPSDVPPTMAVKFLGAAGTACFDLVTFPDTAKVRLIOGENDAVGTARLVYRG 60



QY 61 VLGTTITWVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSSLTTRI 120  
DB 61 VLGTTITWVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSSLTTRI 120  
QY 121 LAGCTTGAAVTCAGPTDVVKVRFQASIHLSGSRSDRKSGTMDARTTAREEGVGLMK 180  
DB 121 LAGCTTGAAVTCAGPTDVVKVRFQASIHLSGSRSDRKSGTMDARTTAREEGVGLMK 180  
QY 181 GTLPNIMRAIVNCAEVVYTDILKEKLDYHLTNDPCHFYSAFAGFCATVVASPVUV 240  
DB 181 GTLPNIMRAIVNCAEVVYTDILKEKLDYHLTNDPCHFYSAFAGFCATVVASPVUV 240  
QY 241 VETRYNNSPPGOYFSPFLDCMIMVNAOEGPTAFYKGFPSFLRGSNNVVMFTYEQLKRA 300  
DB 241 VETRYNNSPPGOYFSPFLDCMIMVNAOEGPTAFYKGFPSFLRGSNNVVMFTYEQLKRA 300  
QY 301 LMKVQMLRESPP 312  
DB 301 LMKVQMLRESPP 312

## RESULT 2

US-09-826-507-2  
; Sequence 2, Application US/09826507  
; Patent No. US2002004492A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee James Beasley  
; APPLICANT: John Christopher Clapham  
; APPLICANT: Robert James Godden  
; TITLE OF INVENTION: NEW USE  
; FILE REFERENCE: GH-30009-C1  
; CURRENT APPLICATION NUMBER: US/09/826,507  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/312,620  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 9814926.3  
; PRIOR FILING DATE: 1998-07-09  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-826-507-2

Query Match 100.0%; Score 1620; DB 9; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.2e-167; Indels 0; Gaps 0;  
Matches 312; Conservative 0; Mismatches 0;

QY 1 MGLKPSDVPPTMAKFIAGTACFADLVTPPLDTAKVRLQIOGENAVQTARLVQYRG 60  
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DB 61 VLGTTITWVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSSLTTRI 120  
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DB 121 LAGCTTGAAVTCAGPTDVVKVRFQASIHLSGSRSDRKSGTMDARTTAREEGVGLMK 180  
QY 181 GTLPNIMRAIVNCAEVVYTDILKEKLDYHLTNDPCHFYSAFAGFCATVVASPVUV 240  
DB 181 GTLPNIMRAIVNCAEVVYTDILKEKLDYHLTNDPCHFYSAFAGFCATVVASPVUV 240  
QY 241 VETRYNNSPPGOYFSPFLDCMIMVNAOEGPTAFYKGFPSFLRGSNNVVMFTYEQLKRA 300  
DB 241 VETRYNNSPPGOYFSPFLDCMIMVNAOEGPTAFYKGFPSFLRGSNNVVMFTYEQLKRA 300  
QY 301 LMKVQMLRESPP 312  
DB 301 LMKVQMLRESPP 312

## RESULT 3

US-09-808-457-2  
; Sequence 2, Application US/09808457  
; Patent No. US20020065239A1  
; GENERAL INFORMATION:  
; APPLICANT: Boetcheer, Brian  
; APPLICANT: Caplan, Shari  
; APPLICANT: Kaleko, Michael  
; APPLICANT: Connelly, Sheila  
; APPLICANT: Desai, Urv  
; APPLICANT: Slobergy, Eric  
; TITLE OF INVENTION: Methods and Compositions for Treatment  
; FILE REFERENCE: 4-31353A/USN  
; CURRENT APPLICATION NUMBER: US/09/808,457  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/XXX,XXX  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Protein UCP3L  
US-09-808-457-2

Query Match 100.0%; Score 1620; DB 9; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.2e-167; Indels 0; Gaps 0;  
Matches 312; Conservative 0; Mismatches 0;

QY 1 MGLKPSDVPPTMAKFIAGTACFADLVTPPLDTAKVRLQIOGENAVQTARLVQYRG 60  
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QY 61 VLGTTITWVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSSLTTRI 120  
DB 61 VLGTTITWVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSSLTTRI 120  
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DB 121 LAGCTTGAAVTCAGPTDVVKVRFQASIHLSGSRSDRKSGTMDARTTAREEGVGLMK 180  
QY 181 GTLPNIMRAIVNCAEVVYTDILKEKLDYHLTNDPCHFYSAFAGFCATVVASPVUV 240  
DB 181 GTLPNIMRAIVNCAEVVYTDILKEKLDYHLTNDPCHFYSAFAGFCATVVASPVUV 240  
QY 241 VETRYNNSPPGOYFSPFLDCMIMVNAOEGPTAFYKGFPSFLRGSNNVVMFTYEQLKRA 300  
DB 241 VETRYNNSPPGOYFSPFLDCMIMVNAOEGPTAFYKGFPSFLRGSNNVVMFTYEQLKRA 300  
QY 301 LMKVQMLRESPP 312  
DB 301 LMKVQMLRESPP 312

## RESULT 4

US-10-671-628-9  
; Sequence 9, Application US/10671628  
; Publication No. US20040068105A1  
; GENERAL INFORMATION:  
; APPLICANT: ITO, Kikukatsu  
; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins  
; FILE REFERENCE: 2003-1386A/WAC/00653  
; CURRENT APPLICATION NUMBER: US/10/671,628  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: 10/009,962  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: PCT/JP00/03806  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: JP11-167439

PRIOR FILING DATE: 1999-06-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-671-628-9

Query Match 100.0%; Score 1620; DB 12; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2,2e-167;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VLGTILTMVTEGCPSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGDNSLTTRI 120  
DB 61 VLGTILTMVTEGCPSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGDNSLTTRI 120  
QY 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSDRKYSGTMDAYRTIAREEGVRLMK 180  
DB 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSDRKYSGTMDAYRTIAREEGVRLMK 180  
QY 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPVDV 240  
DB 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPVDV 240  
QY 241 VKTRYNMSPGQYFSPDLCMIKMAVQEGPTAFYKGFPSFLRLGSMNVVFVTEQLKRA 300  
DB 241 VKTRYNMSPGQYFSPDLCMIKMAVQEGPTAFYKGFPSFLRLGSMNVVFVTEQLKRA 300  
QY 301 LMKVQMLRESPE 312  
DB 301 LMKVQMLRESPE 312

## RESULT 5

US-10-270-861-35  
Sequence 35, Application US/10270861  
Publication No. US2003007749A1  
GENERAL INFORMATION:  
APPLICANT: Pan, James  
APPLICANT: Adams, Sean  
TITLE OF INVENTION: UCP5  
FILE REFERENCE: P1663R2  
CURRENT APPLICATION NUMBER: US/10/270, 861  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: US/09/433, 622  
PRIOR FILING DATE: 1999-11-02  
PRIOR APPLICATION NUMBER: US 60/110, 286  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: US 60/129, 583  
PRIOR FILING DATE: 1999-04-16  
PRIOR APPLICATION NUMBER: US 60/143, 886  
PRIOR FILING DATE: 1999-07-15  
NUMBER OF SEQ ID NOS: 36  
SEQ ID NO 35  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-270-861-35

Query Match 96.0%; Score 1556; DB 14; Length 300;  
Best Local Similarity 100.0%; Pred. No. 1,9e-160;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MAVFELAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRGVLTILTMVTE 72  
DB 1 MAVFELAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRGVLTILTMVTE 72  
QY 73 GPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGDNSLTTRIAGCTTGAMAVT 132

DB 61 GPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGDNSLTTRIAGCTTGAMAVT 120  
QY 133 CAOPTDVVKVRFQASIHGSPSRSDRKYSGTMDAYRTIAREEGVRLMKGLPIMIRNAIV 192  
DB 121 CAOPTDVVKVRFQASIHGSPSRSDRKYSGTMDAYRTIAREEGVRLMKGLPIMIRNAIV 180  
QY 193 NCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPVDVVKTRYNMSPGQ 252  
DB 181 NCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPVDVVKTRYNMSPGQ 240  
QY 253 YFSPDLCMIKMAVQEGPTAFYKGFPSFLRLGSMNVVFVTEQLKRALMKVQMLRESPE 312  
DB 241 YFSPDLCMIKMAVQEGPTAFYKGFPSFLRLGSMNVVFVTEQLKRALMKVQMLRESPE 300

## RESULT 6

US-09-808-457-4  
Sequence 4, Application US/09808457  
Patent No. US20020065239A1  
GENERAL INFORMATION:  
APPLICANT: Boettcher, Brian  
APPLICANT: Caplan, Shari  
APPLICANT: Kaleko, Michael  
APPLICANT: Connolly, Sheila  
APPLICANT: Desai, Urvil  
APPLICANT: Slosberg, Eric  
TITLE OF INVENTION: Methods and Compositions For Treatment  
of Diabetes and Related Conditions Via Gene Therapy  
FILE REFERENCE: 4-31353A/USN  
CURRENT APPLICATION NUMBER: US/09/808, 457  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/xxx,xxx  
PRIOR FILING DATE: 2000-03-15  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq For Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 275  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Protein UCP35  
US-09-808-457-4

Query Match 88.3%; Score 1430; DB 9; Length 275;  
Best Local Similarity 100.0%; Pred. No. 8,7e-147;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLGKPSDVPPTMAVKELGAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRG 60  
DB 1 MVLGKPSDVPPTMAVKELGAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRG 60  
QY 61 VLGTILTMVTEGCPSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGDNSLTTRI 120  
DB 61 VLGTILTMVTEGCPSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGDNSLTTRI 120  
QY 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSDRKYSGTMDAYRTIAREEGVRLMK 180  
DB 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSDRKYSGTMDAYRTIAREEGVRLMK 180  
QY 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPVDV 240  
DB 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPVDV 240  
QY 241 VKTRYNMSPGQYFSPDLCMIKMAVQEGPTAFYKGFPSFLRLGSMNVVFVTEQLKRALMKVQMLRESPE 312  
DB 241 VKTRYNMSPGQYFSPDLCMIKMAVQEGPTAFYKGFPSFLRLGSMNVVFVTEQLKRALMKVQMLRESPE 300

## RESULT 7

US-09-823-886A-6  
Sequence 6, Application US/09823886A  
Publication No. US20030150022A1

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GENERAL INFORMATION:
APPLICANT: Berry-Lowe, Martha
TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
FILE REFERENCE: C1102/7002
CURRENT APPLICATION NUMBER: US/09/823,886A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,533
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 284
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-886A-6

Query Match      88.3% Score 1430; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 9,1e-147;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60
DB 10 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 69
QY 61 VLGITLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTIRI 120
DB 70 VLGITLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTIRI 129
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSDRKXSGTMDAYRTIAREEGVRLGW 180
DB 130 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSDRKXSGTMDAYRTIAREEGVRLGW 189
QY 181 GTLENMKNALVNCALVYVTDILKEKLDYHLTDNPFCHFSAGAGFCATVVASPDV 240
DB 190 GTLENMKNALVNCALVYVTDILKEKLDYHLTDNPFCHFSAGAGFCATVVASPDV 249
QY 241 VKTRMNSPPGOYFSPIDCMIMVVAOEGPTAFYKG 275
DB 250 VKTRMNSPPGOYFSPIDCMIMVVAOEGPTAFYKG 284

RESULT 8
US-09-884-814-8
Sequence 8, Application US/09884814
Patent No. US20020127600A1
GENERAL INFORMATION:
APPLICANT: Chen, Jin-Long
APPLICANT: Amaral, M. Catherine
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Human uncoupling protein 2 (hUCP2): Compositions and
METHODS OF INVENTION: Methods of use
FILE REFERENCE: 018781-001110US
CURRENT APPLICATION NUMBER: US/09/884,814
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 09/124,293
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.
US-09-884-814-8

Query Match      71.1% Score 1152.5; DB 9; Length 309;
Best Local Similarity 72.2%; Pred. No. 1.6e-116;
Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;

QY 1 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYR 59
DB 1 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYR 59

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DB 61 GVMGTTLMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTIR 119
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DB 120 ILAAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSDRKXSGTMDAYRTIAREEGVRLGW 176
QY 180 KGTLENMKNALVNCALVYVTDILKEKLDYHLTDNPFCHFSAGAGFCATVVASPDV 239
DB 177 KGTLENMKNALVNCALVYVTDILKEKLDYHLTDNPFCHFSAGAGFCATVVASPDV 236
QY 240 VKTRMNSPPGOYFSPIDCMIMVVAOEGPTAFYKGFTPSFLRGSVMVVFVTEQOLKR 299
DB 237 VKTRMNSPPGOYFSPIDCMIMVVAOEGPTAFYKGFTPSFLRGSVMVVFVTEQOLKR 296
QY 300 ALMKVQLRESPP 312
DB 297 ALMAACTSREAPF 309

RESULT 9
US-10-001-051B-2
Sequence 2, Application US/10001051B
Patent No. US20020172958A1
GENERAL INFORMATION:
APPLICANT: Gonzalez-Zulueta, Mirella
APPLICANT: Shamloo, Mehdiad
APPLICANT: McFarland, K.C.
APPLICANT: Chin, Daniel
APPLICANT: Weloeb, Tadeusz
APPLICANT: Melcher, Thorsten
TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING
METHODS OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
FILE REFERENCE: 019488-003010US
CURRENT APPLICATION NUMBER: US/10/001,051B
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/244,946
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 309
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Any animal
US-10-001-051B-2

Query Match      71.1% Score 1152.5; DB 13; Length 309;
Best Local Similarity 72.2%; Pred. No. 1.6e-116;
Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;

QY 1 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYR 59
DB 1 MWGFKATDVPPTAVKFLGAGTACIADLITPPLDTAKVRLQIOGESQGPVATASAGYR 60
QY 60 GVLGTTLMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTIR 119
DB 61 GVMGTTLMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTIR 119
QY 120 ILAAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSDRKXSGTMDAYRTIAREEGVRLGW 179
DB 120 ILAAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPRSDRKXSGTMDAYRTIAREEGVRLGW 176
QY 180 KGTLENMKNALVNCALVYVTDILKEKLDYHLTDNPFCHFSAGAGFCATVVASPDV 239
DB 177 KGTLENMKNALVNCALVYVTDILKEKLDYHLTDNPFCHFSAGAGFCATVVASPDV 236

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QY 240 VVKTRVNSPPGOYSPPLDCMKVVAOEGPTAFYKGFPSFLRSGSNVVMFVYEQLR 299  
 DB 237 VVKTRVNSALGOYSAGHCALTMLOKEGPRAFYKGFMSFLRSGSNVVMFVYEQLR 296  
 QY 300 ALMKVQMLRESPF 312  
 DB 297 ALMAACTSREAPF 309

RESULT 10  
 US-10-197-019-3  
 ; Sequence 3, Application US/10197019  
 ; Publication No. US20030207284A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chew, Anne  
 ; APPLICANT: Denton, R. Rex  
 ; APPLICANT: Gilson, Christopher Raleigh  
 ; APPLICANT: Nandabalan, Krishnan  
 ; APPLICANT: Parks, Katie B.  
 ; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE  
 ; FILE REFERENCE: MMH-004205  
 ; CURRENT APPLICATION NUMBER: US/10/197, 019  
 ; PRIOR FILING DATE: 2002-07-16  
 ; PRIOR APPLICATION NUMBER: PCT/US01/02485  
 ; PRIOR FILING DATE: 2001-01-25  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 309  
 ; TYPE: PRF  
 ; ORGANISM: Homo sapiens  
 ; US-10-197-019-3

Query Match 71.1%; Score 1152.5; DB 15; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 1.5e-116; Indels 5; Gaps 3;  
 Matches 226; Conservative 32; Mismatches 50;

QY 1 MYGLKPSDVPPTMAVKEFLGAGTAACPADLVTPPLDTAKVRLQIOGNSQA-VQTAFLVQYR 59  
 DB 1 MGFPAKTDVPPATVYKFLGAGTAACPADLVTPPLDTAKVRLQIOGNSQGPVATASQYR 60  
 QY 60 GVLGTLTWRTGEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTR 119  
 DB 61 GVMGTLTWRTGEGPSRLYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTR 119  
 QY 120 ILAGCTGMAVYTCAPTDVVKVRPQASIHLSRSDRYSGMTDAYRTIAREEGVRLW 179  
 DB 120 LLAGSTTGALAAVAPTDVVKVRPQQAQABAG--GGRRYOSTVNAVKTIAEEGFRGLW 176  
 QY 180 KGTLPVIMENAIYVNCAEVYTYDILKEKLDYHLITDNFCHFPVSAGAGFCATVVASPD 239  
 DB 177 KGTSPVARNAIYVNCHELVYTDILKALKAMLTDDLCHFTSAGAGCTTVIASPD 236  
 QY 240 VVKTRVNSPPGOYSPPLDCMKVVAOEGPTAFYKGFPSFLRSGSNVVMFVYEQLR 299  
 DB 237 VVKTRVNSALGOYSAGHCALTMLOKEGPRAFYKGFMSFLRSGSNVVMFVYEQLR 296  
 QY 300 ALMKVQMLRESPF 312  
 DB 297 ALMAACTSREAPF 309

RESULT 11  
 US-09-884-814-1  
 ; Sequence 1, Application US/09884814  
 ; Patent No. US20020127600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jin-Long  
 ; APPLICANT: Amaral, M. Catherine  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and  
 ; METHODS OF USE  
 ; FILE REFERENCE: 018781-001110US

QY 1 CURRENT APPLICATION NUMBER: US/09/884,814  
 DB 1 CURRENT FILING DATE: 2001-06-18  
 QY 1 PRIOR APPLICATION NUMBER: US 09/124,293  
 DB 1 PRIOR FILING DATE: 1998-07-29  
 QY 1 NUMBER OF SEQ ID NOS: 8  
 DB 1 SOFTWARE: PatentIn Ver. 2.1  
 QY 1 SEQ ID NO 1  
 DB 1 LENGTH: 309  
 QY 1 TYPE: PRF  
 DB 1 ORGANISM: Homo sapiens  
 QY 1 FEATURE:  
 DB 1 OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)  
 ; US-09-884-814-1

Query Match 71.0%; Score 1149.5; DB 9; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 3.5e-116;  
 Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MYGLKPSDVPPTMAVKEFLGAGTAACPADLVTPPLDTAKVRLQIOGNSQA-VQTAFLVQYR 59  
 DB 1 MGFPAKTDVPPATVYKFLGAGTAACPADLVTPPLDTAKVRLQIOGNSQGPVATASQYR 60  
 QY 60 GVLGTLTWRTGEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTR 119  
 DB 61 GVMGTLTWRTGEGPSRLYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTR 119  
 QY 120 ILAGCTGMAVYTCAPTDVVKVRPQASIHLSRSDRYSGMTDAYRTIAREEGVRLW 179  
 DB 120 LLAGSTTGALAAVAPTDVVKVRPQQAQABAG--GGRRYOSTVNAVKTIAEEGFRGLW 176  
 QY 180 KGTLPVIMENAIYVNCAEVYTYDILKEKLDYHLITDNFCHFPVSAGAGFCATVVASPD 239  
 DB 177 KGTSPVARNAIYVNCHELVYTDILKALKAMLTDDLCHFTSAGAGCTTVIASPD 236  
 QY 240 VVKTRVNSPPGOYSPPLDCMKVVAOEGPTAFYKGFPSFLRSGSNVVMFVYEQLR 299  
 DB 237 VVKTRVNSALGOYSAGHCALTMLOKEGPRAFYKGFMSFLRSGSNVVMFVYEQLR 296  
 QY 300 ALMKVQMLRESPF 312  
 DB 297 ALMAACTSREAPF 309

RESULT 12  
 US-10-336-472-132  
 ; Sequence 132, Application US/10336472  
 ; Publication No. US20040043929A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Ballinger, Robert A.  
 ; APPLICANT: Baumgartner, Jason C.  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Chant, John S.  
 ; APPLICANT: Bergins, Constance  
 ; APPLICANT: Gangolli, Saba A.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Furtak, Katarzyna  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Gilber, Jennifer A.  
 ; APPLICANT: Gunther, Erik  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Jia, Weizhen  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Padigara, Muralidhara  
 ; APPLICANT: Patunajan, Meera  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: MacDougall, John R.

```

APPLICANT: Mishra, Vishnu
APPLICANT: Pena, Carol E.A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Shinkets, Richard A.
APPLICANT: Smithson, Glenda
APPLICANT: Spytek, Kimberly A.
APPLICANT: Stone, David J.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Ort, Tatiana
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.M.
APPLICANT: Wolenc, Adam R.
APPLICANT: Zernusen, Bryan D.
APPLICANT: Zhong, Mei
FILE REFERENCE: 21402-533C
CURRENT APPLICATION NUMBER: US/10/336,472
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/005,041
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 10/023,681
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 10/024,212
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 10/080,334
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/092,900
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 10/136,826
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: 10/236,417
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/345,092
PRIOR FILING DATE: 2002-01-04
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 230
SOFTWARE: CureseqList version 0.1
SEQ ID NO 132
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-336-472-132

Query Match      71.0%; Score 1149.5; DB 12; Length 309;
Best Local Similarity 72.2%; Pred. No. 3.5e-116;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MVLKPSDVPPTMAVFLGAGTAACFADLVTPPLDTAKVRLQIOGENOA-VQTARLVQYR 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGFATDVPPPTATVFLGAGTAACIADLITPLDTAKVRLQIOGSGPVRATASAOYR 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 GVLGTLTMMVRTEGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYVTEPKGADNSLTTR 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GVMGTLTMMVRTEGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYVTEPKGADNSLTTR 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 ILAGCTTGMAVTCAPPTDVVVRFOASIHGSPSRSDKSGTMDAYRTIAREEGVRLG 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 ILAGCTTGMAVTCAPPTDVVVRFOASIHGSPSRSDKSGTMDAYRTIAREEGVRLG 176
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 180 KGTLPNIMRNAIVNCAEVVTVYDILKEKLDYHLTNDNPFCHPVASGAGFCATVVASPV 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 177 KGTSPVANAIVNCAELVTVYDILKDALLKANMTDLPCHFTSAGAGFCCTVVIASPV 236
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 VKTRYNMSPPGQYFSPDLCKIMVAOEGPTAFYKGFSPFLRLGSMNVVMFTYEQLR 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 237 VKTRYNMSPPGQYFSPDLCKIMVAOEGPTAFYKGFSPFLRLGSMNVVMFTYEQLR 236
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 ALMKVQMLRESPP 312
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 300 ALMKVQMLRESPP 312
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 297 ALMAACTSREAPF 309
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RESULT 13
US-10-671-628-8
Sequence 8, Application US/10671628
Publication No. US20040068105E1
GENERAL INFORMATION:
APPLICANT: ITO, Kikukatsu
FILE REFERENCE: 2003-13864/WMC/00653
CURRENT APPLICATION NUMBER: US/10/671,628
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: 10/009,962
PRIOR FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: PCT/JP00/03806
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: JP11-167439
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-671-628-8

Query Match      71.0%; Score 1149.5; DB 12; Length 309;
Best Local Similarity 72.2%; Pred. No. 3.5e-116;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MVLKPSDVPPTMAVFLGAGTAACFADLVTPPLDTAKVRLQIOGENOA-VQTARLVQYR 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGFATDVPPPTATVFLGAGTAACIADLITPLDTAKVRLQIOGSGPVRATASAOYR 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 GVLGTLTMMVRTEGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYVTEPKGADNSLTTR 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GVMGTLTMMVRTEGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYVTEPKGADNSLTTR 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 ILAGCTTGMAVTCAPPTDVVVRFOASIHGSPSRSDKSGTMDAYRTIAREEGVRLG 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 ILAGCTTGMAVTCAPPTDVVVRFOASIHGSPSRSDKSGTMDAYRTIAREEGVRLG 176
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 180 KGTLPNIMRNAIVNCAEVVTVYDILKEKLDYHLTNDNPFCHPVASGAGFCATVVASPV 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 177 KGTSPVANAIVNCAELVTVYDILKDALLKANMTDLPCHFTSAGAGFCCTVVIASPV 236
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 VKTRYNMSPPGQYFSPDLCKIMVAOEGPTAFYKGFSPFLRLGSMNVVMFTYEQLR 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 237 VKTRYNMSPPGQYFSPDLCKIMVAOEGPTAFYKGFSPFLRLGSMNVVMFTYEQLR 236
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 ALMKVQMLRESPP 312
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 297 ALMAACTSREAPF 309
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-10-270-861-34
Sequence 34, Application US/10270861
Publication No. US2003007749A1
GENERAL INFORMATION:
APPLICANT: Adame, Sean
APPLICANT: Fan, James
FILE REFERENCE: P1663R2
CURRENT APPLICATION NUMBER: US/10/270,861
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US/09/433,622
PRIOR FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: US 60/110,286
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: US 60/129,583

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PRIOR FILING DATE: 1999-04-16  
PRIOR APPLICATION NUMBER: US 60/143,886  
PRIOR FILING DATE: 1999-07-15  
NUMBER OF SEQ ID NOS: 36  
SEQ ID NO 34  
LENGTH: 309  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-270-861-34

Query Match 71.0%; Score 1149.5; DB 14; Length 309;  
Best Local Similarity 72.2%; Pred. No. 3.5e-116;  
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MVLKPSDVPPTMAVKELGAGTAACFADLVTFPLDTAKVRLQIQGSEQGVPRATASQYR 59  
DB 1 MGVFKATDVPPTATVTKFLGAGTAACTADLITFPLDTAKVRLQIQGSEQGVPRATASQYR 60  
QY 60 GVLGTTITWRTREGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKADNSLITR 119  
DB 61 GVMGTTITWRTREGPSRLYNGLVAGLQROMSPASVRIGLYDSVKQFYT-KGSEHASIGSR 119  
QY 120 ILAGCTTGAMAVYCAOPTDVVKVRFOASIHGSPRSDBKSGTMDAYRTIAREEGVRLW 179  
DB 120 LLGSTTGALAVAVAOPTDVVKVRFOAQAPAG--GGRRTQSTVNAVKTIAREEGFRGLW 176  
QY 180 KGTLPNIMRNAIVNCAEVVYTDILKEKLDYHLTDNFPCHFVSAGFCATVVASPVD 239  
DB 177 KGTSPVARNALVNCALVYTDILKDALIKANLMTDDLPCFTSAFGAGCTTIVIASPVD 236  
QY 240 VVKTRYNSPPGOYFSPDCKIMVAOEGPTAFYKGFPSFLRGSNNVVMFVTEQLKR 299  
DB 237 VVKTRYNSALGGYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRGSNNVVMFVTEQLKR 296  
QY 300 ALMKVQMLRESPP 312  
DB 297 ALMAACTSREAPF 309

RESULT 15  
US-10-265-689-1  
Sequence 1, Application US/10265689  
Publication No. US20030119775A1  
GENERAL INFORMATION:  
APPLICANT: SURWIT, RICHARD S.  
APPLICANT: COLLINS, SHEILA A.  
APPLICANT: WARDEN, CRAIG H.  
APPLICANT: SEIDIN, MICHAEL F.  
APPLICANT: RICOTER, DANIEL  
APPLICANT: BOUILLAUD, FREDERIC  
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN  
FILE REFERENCE: 1579-376  
CURRENT APPLICATION NUMBER: US/10/265,689  
CURRENT FILING DATE: 2002-10-08  
PRIOR APPLICATION NUMBER: US/09/353,645  
PRIOR FILING DATE: 1999-07-15  
PRIOR APPLICATION NUMBER: PCT/US97/06864  
PRIOR FILING DATE: 1997-04-22  
PRIOR APPLICATION NUMBER: 60/034,960  
PRIOR FILING DATE: 1997-01-15  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 309  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-265-689-1

Query Match 71.0%; Score 1149.5; DB 14; Length 309;  
Best Local Similarity 72.2%; Pred. No. 3.5e-116;  
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;  
QY 1 MVLKPSDVPPTMAVKELGAGTAACFADLVTFPLDTAKVRLQIQGSEQGVPRATASQYR 59

DB 1 MGVFKATDVPPTATVTKFLGAGTAACTADLITFPLDTAKVRLQIQGSEQGVPRATASQYR 60  
QY 60 GVLGTTITWRTREGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKADNSLITR 119  
DB 61 GVMGTTITWRTREGPSRLYNGLVAGLQROMSPASVRIGLYDSVKQFYT-KGSEHASIGSR 119  
QY 120 ILAGCTTGAMAVYCAOPTDVVKVRFOASIHGSPRSDBKSGTMDAYRTIAREEGVRLW 179  
DB 120 LLGSTTGALAVAVAOPTDVVKVRFOAQAPAG--GGRRTQSTVNAVKTIAREEGFRGLW 176  
QY 180 KGTLPNIMRNAIVNCAEVVYTDILKEKLDYHLTDNFPCHFVSAGFCATVVASPVD 239  
DB 177 KGTSPVARNALVNCALVYTDILKDALIKANLMTDDLPCFTSAFGAGCTTIVIASPVD 236  
QY 240 VVKTRYNSPPGOYFSPDCKIMVAOEGPTAFYKGFPSFLRGSNNVVMFVTEQLKR 299  
DB 237 VVKTRYNSALGGYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRGSNNVVMFVTEQLKR 296  
QY 300 ALMKVQMLRESPP 312  
DB 297 ALMAACTSREAPF 309

Search completed: May 17, 2004, 11:59:18  
Job time : 49 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:49:15 ; Search time 59 Seconds  
(without alignments)  
1494.150 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620  
Sequence: 1 MVLGKPSDVPPTMAVKFLGA.....TYEQLKALMKYQWLRESPP 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_29Jan04:\*

1: geneeqp1980s:\*\*\*  
2: geneeqp1990s:\*\*\*  
3: geneeqp2000s:\*\*\*  
4: geneeqp2001s:\*\*\*  
5: geneeqp2002s:\*\*\*  
6: geneeqp2003s:\*\*\*  
7: geneeqp2003bs:\*\*\*  
8: geneeqp2004s:\*\*\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	100.0	312	2	AAW83379 Human unc
2	1620	100.0	312	2	AAW68197 Human unc
3	1620	100.0	312	2	AAW85667 Human UCP
4	1620	100.0	312	2	AAW88279 Human unc
5	1620	100.0	312	2	AAW31904 Human unc
6	1620	100.0	312	3	AAW54600 Amino ac
7	1620	100.0	312	3	AAW44253 Human mlt
8	1620	100.0	312	4	AAW74296 Human UCP
9	1620	100.0	312	4	AAE04298 Human unc
10	1620	100.0	312	4	AAW68050 Amino ac
11	1620	100.0	312	5	AAW81610 UCP3L pro
12	1620	100.0	312	5	AAE19348 Human mlt
13	1620	100.0	312	7	AAW54391 Human Pro
14	1616	99.8	312	2	AAW81587 Human unc
15	1610	99.4	312	2	AAW81588 Protein e
16	1430	88.3	275	3	AAW63380 Human unc
17	1430	88.3	275	3	AAW44293 Human unc
18	1430	88.3	275	4	AAW72343 Human unc
19	1430	88.3	275	5	AAW81611 UCP3S pro
20	1430	88.3	284	4	AAW09078 Human unc
21	1426	88.0	275	2	AAW81591 Human unc
22	1403.5	86.6	339	2	AAW81592 Protein e
23	1373	84.8	308	2	AAW81595 Mouse unc
24	1373	84.8	308	2	AAW88280 Mouse unc
25	1369	84.5	308	2	AAW29834 Mouse unc

26	1369	84.5	308	2	AAW85116	AAW85116 A murine
27	1369	84.5	308	2	AAW77452	AAW77452 Murine mi
28	1369	84.5	308	4	AAE04729	AAE04729 Mouse unc
29	1366	84.3	397	2	AAW81596	AAW81596 Protein e
30	1341	82.8	432	2	AAW29835	AAW29835 Mouse unc
31	1341	82.8	432	2	AAW85117	AAW85117 A murine
32	1341	82.8	432	3	AAW77453	AAW77453 Murine mi
33	1341	82.8	432	4	AAE04730	AAE04730 Mouse unc
34	1156.5	71.4	309	7	AAW54389	AAW54389 Rat Prote
35	1152.5	71.1	309	2	AAW69166	AAW69166 Human res
36	1152.5	71.1	309	2	AAW28352	AAW28352 UCP2 amn
37	1152.5	71.1	309	5	AAW98901	AAW98901 Human unc
38	1149.5	71.0	309	2	AAW28351	AAW28351 UCP2 amn
39	1149.5	71.0	309	2	AAW31903	AAW31903 Human unc
40	1149.5	71.0	309	3	AAW44292	AAW44292 Human unc
41	1149.5	71.0	309	3	AAW45002	AAW45002 Tularik h
42	1149.5	71.0	309	4	AAW72342	AAW72342 Human unc
43	1149.5	71.0	309	4	AAW09077	AAW09077 Human unc
44	1147.5	70.8	309	2	AAW24000	AAW24000 Complete
45	1147.5	70.8	309	2	AAW89546	AAW89546 Full leng

#### ALIGNMENTS

RESULT 1.  
AAW83379 standard; protein; 312 AA.  
ID AAW83379  
AC AAW83379;  
DT 22-FEB-1999 (first entry)  
DE Human uncoupling protein UCP3L.  
XX  
XX  
XX Human; uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation;  
KW adenosine triphosphate; mitochondria; skeletal muscle; gene therapy;  
KW thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;  
KW insulin sensitivity; neuromuscular disease.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO98050542-A1.  
XX  
XX 12-NOV-1998.  
XX  
XX 05-MAY-1998; 98WO-EP002645.  
XX  
XX 07-MAY-1997; 97CH-00001072.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
XX Giacobino J, Muzzin P, Boes O;  
XX  
XX WPI; 1998-610382/51.  
XX DR N-PSDB; AAW72690.  
XX  
XX New human skeletal muscle uncoupling proteins UCP3L and UCP3S - useful  
XX PT for controlling thermogenesis in human skeletal muscle and heart, e.g.  
XX PT for treating obesity and cachexia.  
XX  
XX  
XX  
XX Claim 5; Page 15-16; 26pp; English.  
XX  
XX The present sequence represents human uncoupling protein UCP3L. UCP3  
XX uncouples oxidative phosphorylation and synthesis of adenosine  
XX triphosphate in the mitochondria of skeletal muscle. The coding sequences  
XX for UCP3L and UCP3S are useful for gene therapy of dysfunctions of  
XX thermogenesis in human skeletal muscle and heart which result from a lack  
XX of UCP3 and which can induce disorders such as obesity or cachexia.  
XX Antisense oligonucleotides to UCP3L and UCP3S can be used for correcting  
XX an excess of UCP3. Modification of endogenous UCP3 activity (using  
XX activators or inhibitors of UCP3) is used to induce bodyweight loss (loss

CC of adipose mass and maintenance of the lean mass) in all types of obesity  
 CC by promoting the dissipation of energy; for preventing an excessive  
 CC weight regain following restrictive food diet or after ceasing a physical  
 CC training programme; for preventing and treating type II diabetes by  
 CC improving sensitivity to insulin; for preventing hypertension; for  
 CC increasing muscle mass in states of cachexia; for treatment of  
 CC insufficiencies or disturbances of cardiac rhythm due to a dysfunction of  
 CC UCP3; and for the treatment of neuromuscular diseases due to a  
 CC dysfunction of UCP3. The uncoupling proteins can also be used to raise  
 CC antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows  
 CC generation of transgenic animals, e.g. for screening substances which  
 CC modify UCP3 expression or activity or for investigating the biological  
 CC role of UCP3

CC Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 2; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 DB 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 QY 61 VLGITLTWRTGEGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTRI 120  
 DB 61 VLGITLTWRTGEGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTRI 120  
 QY 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 DB 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 QY 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 DB 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 QY 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVDV 240  
 DB 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVDV 240  
 QY 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 DB 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 QY 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 DB 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 QY 301 LMKVQMLRESPP 312  
 DB 301 LMKVQMLRESPP 312

#### RESULT 2

ID AAM68197 standard; protein; 312 AA.

AAW68197;

07-DEC-1998 (first entry)

Human uncoupling protein HNF6W60.

HNFCW60; uncoupling protein; human; body weight disorder; obesity;  
 diabetes; hyperlipidaemia; diagnosis; therapy; vaccine.

OS Homo sapiens.

PN WO9839432-A1.

PD 11-SEP-1998.

PP 02-MAR-1998; 98WO-GB000633.

PR 05-MAR-1997; 97GB-00004551.

PR 18-MAR-1997; 97GB-00005614.

PR 16-JUL-1997; 97EP-00305305.

PA (SMK ) SMITHKLINE BEECHAM PLC.

XX Beeley LJ, Paine K, Godden RJ;

XX WPI; 1998-495841/42.  
 DR N-PSDB; AAV54602.  
 XX  
 PT New isolated human uncoupling poly(peptide)s - used to develop products  
 PT for the diagnosis, prevention and treatment of body weight disorders,  
 PT obesity and diabetes.

PS Claim 4; Page 24-25; 41pp; English.

CC This is the amino acid sequence of novel human uncoupling protein  
 CC HNF6W60, as deduced from an isolated polynucleotide (see AAV54602). The  
 CC invention relates to HNF6W60 polypeptides and recombinant materials and  
 CC methods for their production. It also relates to methods for using such  
 CC HNF6W60 polypeptides and polynucleotides. Such uses include the treatment  
 CC of obesity, diabetes, hyperlipidaemia and body weight disorders. The  
 CC invention also provides methods of identifying agonists and antagonists,  
 CC and methods for treating conditions associated with HNF6W60 imbalance  
 CC using the identified compounds. In addition, diagnostic assays for  
 CC detecting diseases associated with inappropriate HNF6W60 activity or  
 CC levels are provided

CC Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 2; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 DB 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 QY 61 VLGITLTWRTGEGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTRI 120  
 DB 61 VLGITLTWRTGEGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSSLTTRI 120  
 QY 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 DB 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 QY 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 DB 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180  
 QY 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVDV 240  
 DB 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVDV 240  
 QY 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 DB 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 QY 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 DB 241 VETRYNNSPPGOYFSPFLDCMIMVAQEGPTAFYKGFPSFLRSGSNVVMFVYEQLKRA 300  
 QY 301 LMKVQMLRESPP 312  
 DB 301 LMKVQMLRESPP 312

#### RESULT 3

ID AAW85667 standard; protein; 312 AA.

AAW85667;

19-JUL-1999 (first entry)

Human UCP-3 (uncoupling protein).

UCP-3; uncoupling protein; thermogenesis; skeletal muscle; treatment;  
 obesity; diabetes; hyperthermia; fever; detection; diagnosis.

OS Homo sapiens.

PN WO9845313-A1.

PD 15-OCT-1998.

PP 25-MAR-1998; 98WO-US005892.

```

XX 04-APR-1997; 97US-0043407P.
PR 08-MAY-1997; 97US-0046154P.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Larkin S, Moore C, Albrandt K, Young A, Beaumont K;
XX WPI; 1999-131682/11.
XX N-PSDB; AAX08507.
XX
XX New isolated uncoupling protein, UCP3 - used to develop products for
XX modulating thermogenesis in tissues, e.g. for treating obesity, diabetes,
XX malignant hyperthermia or fever.
XX
XX Claim 4; Fig 5; 97p; English.
XX
XX The uncoupling protein UCP-3 is involved in thermogenesis and energy
XX utilisation in skeletal muscle. The nucleic acid molecule encoding UCP-3
XX or compounds which activate UCP-3 can be used to increase thermogenesis
XX in a subject, e.g. for treating obesity or for decreasing the amount of
XX fat in a subject. They can also be used for treating diabetes. Compounds
XX which inhibit UCP-3 activation in tissues of a subject can be used for
XX decreasing thermogenesis or respiratory ATP synthesis e.g. for preventing
XX or treating malignant hyperthermia or fever. The UCP-3 can also be used
XX for screening for compounds that bind to or modulate the activity of UCP-
XX 3, these compounds can then be used in detection and diagnosis
XX
XX Sequence 312 AA;
XX
XX Query Match 100.0%; Score 1620; DB 2; Length 312;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-165; Indels 0; Gaps 0;
XX Matches 312; Conservative 0; Mismatches 0;
XX
XX 1 MGLKPSDVPPTMAVVFGLAGTAACFADLVTPPLDTAKVRLQIGENQAVQFARLVQYRG 60
XX |||||||
XX 1 MGLKPSDVPPTMAVVFGLAGTAACFADLVTPPLDTAKVRLQIGENQAVQFARLVQYRG 60
XX
XX 61 VGTITLTMVTRTEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPPGADNSSLITTR 120
XX |||||||
XX 61 VGTITLTMVTRTEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPPGADNSSLITTR 120
XX
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX |||||||
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX
XX 181 GTLPNIMRNAIYVCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX |||||||
XX 181 GTLPNIMRNAIYVCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX
XX 241 VKTRYNNSPPGOYFSPFLDCMIMKVAOEGPTAFYKGTPTPSFLRLGSNNVVFVTE 300
XX |||||||
XX 241 VKTRYNNSPPGOYFSPFLDCMIMKVAOEGPTAFYKGTPTPSFLRLGSNNVVFVTE 300
XX
XX 301 LMKVQMLRESPP 312
XX |||||||
XX 301 LMKVQMLRESPP 312
XX
XX RESULT 4
XX ID AAW88279 standard; protein; 312 AA.
XX
XX AAW88279;
XX
XX 12-APR-1999 (first entry)
XX
XX Human uncoupling protein 3 (UCP3).
XX
XX Uncoupling protein 3; UCP3; human; obesity; diabetes; hyperinsulinaemia;
XX hypermetabolism; therapy.
XX
XX Homo sapiens.

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XX MO9852958-A1.
XX
XX 26-NOV-1998.
XX
XX 19-MAY-1998; 98WO-US010215.
XX
XX 20-MAY-1997; 97US-0047179P.
XX 08-AUG-1997; 97GB-00016886.
XX 09-DEC-1997; 97US-0069141P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Liu Q, Chen F;
XX
XX WPI; 1999-059737/05.
XX N-PSDB; AAV84254.
XX
XX New isolated human uncoupling protein 3 - used to identify compounds
XX which can modulate energy expenditure and body weight regulation, e.g. in
XX the treatment of obesity or diabetes.
XX
XX Claim 3; Page 58; 87p; English.
XX
XX This is human uncoupling protein 3 (UCP3), a novel protein that is
XX involved in energy expenditure and body weight regulation and whose
XX expression is mostly limited to skeletal muscle. The amino acid sequence
XX was deduced from the nucleotide sequence of an isolated foetal brain cDNA
XX clone (see AAV84254). The invention additionally provides related
XX recombinant expression vectors and recombinant host cells. UCP3
XX polypeptides and transformed recombinant cell lines can be used for
XX identifying modulators of UCP3 activity. The modulators can be used for
XX treating diseases such as obesity and diabetes, by manipulating the
XX interrelated process of balancing food intake, energy expenditure and
XX glucose metabolism within the patient. They can also be used to treat
XX hyperactive conditions of energy expenditure which originate in the
XX mitochondria of skeletal muscle. UCP3 nucleic acids are useful in gene
XX therapy of obesity and obesity-related indications, including diabetes,
XX and of mitochondrial-associated hypermetabolism
XX
XX Sequence 312 AA;
XX
XX Query Match 100.0%; Score 1620; DB 2; Length 312;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-165; Indels 0; Gaps 0;
XX Matches 312; Conservative 0; Mismatches 0;
XX
XX 1 MGLKPSDVPPTMAVVFGLAGTAACFADLVTPPLDTAKVRLQIGENQAVQFARLVQYRG 60
XX |||||||
XX 1 MGLKPSDVPPTMAVVFGLAGTAACFADLVTPPLDTAKVRLQIGENQAVQFARLVQYRG 60
XX
XX 61 VGTITLTMVTRTEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPPGADNSSLITTR 120
XX |||||||
XX 61 VGTITLTMVTRTEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPPGADNSSLITTR 120
XX
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX |||||||
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX
XX 181 GTLPNIMRNAIYVCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX |||||||
XX 181 GTLPNIMRNAIYVCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX
XX 241 VKTRYNNSPPGOYFSPFLDCMIMKVAOEGPTAFYKGTPTPSFLRLGSNNVVFVTE 300
XX |||||||
XX 241 VKTRYNNSPPGOYFSPFLDCMIMKVAOEGPTAFYKGTPTPSFLRLGSNNVVFVTE 300
XX
XX 301 LMKVQMLRESPP 312
XX |||||||
XX 301 LMKVQMLRESPP 312
XX
XX RESULT 5
XX AAY31904

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ID AAY31904 standard; protein; 312 AA.  
 XX AAY31904;  
 XX 21-DEC-1999 (first entry)  
 XX Human uncoupling protein 3.  
 DE Human uncoupling protein 3.  
 XX  
 KM Uncoupling protein 3; UCP3; human; obesity; diabetes; diagnosis;  
 KM gene therapy.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 70 /note= "substituted by Trp in C208T polymorphism"  
 FT Misc-difference 102 /note= "substituted by Val in G304A polymorphism"  
 FT Misc-difference 142 /note= "C-terminal residue in C427T polymorphism"  
 FT  
 XX W09948905-A1.  
 XX  
 PD 30-SEP-1999.  
 PD  
 PF 23-MAR-1999; 99WO-US006317.  
 XX  
 PR 23-MAR-1999; 98US-0078972P.  
 XX  
 PA (MUSC-) MUSC FOUND RES DEV.  
 XX  
 PI Garvey WT, Argypopoulos G;  
 XX  
 DR WPI; 1999-591072/50.  
 DR N-PSDB; AA219969.  
 XX  
 PT Use of uncoupled protein 2 or 3 as markers for identifying subjects at  
 PT risk of developing obesity or diabetes.  
 XX  
 PS Disclosure; Page 103-104; 112pp; English.  
 XX  
 XX The present sequence represents human uncoupling protein 3 (UCP3). The  
 CC invention relates to the discovery that the presence of a single  
 CC nucleotide polymorphism (SNP) in a nucleic acid encoding UCP3 (see  
 CC AA219969) or UCP2 (see AA219968) can correlate with the development of  
 CC obesity and type II diabetes mellitus. In UCP3, the SNP may generate a  
 CC Trp for Arg substitution at position 70 of the encoded protein, a protein  
 CC truncated after residue 142, or a Val for Ile substitution at position  
 CC 102. Methods are provided for identifying a subject at risk of developing  
 CC obesity and/or diabetes by detection of the SNP in the UCP2 UCP3 nucleic  
 CC acid or amino acid sequence. An antibody to an antigen of the altered  
 CC UCP2 can be used in such a method  
 XX  
 SO Sequence 312 AA;  
 Query Match 100.0%; Score 1620; DB 2; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MWGLKSDVPTMAVFLAGTAACFADLVTPPLDTAKRLQIQENQAVQTARLVQYRG 60  
 DB 1 MWGLKSDVPTMAVFLAGTAACFADLVTPPLDTAKRLQIQENQAVQTARLVQYRG 60  
 QY 61 VGTGTLTMTWRTGSPSPYNGLVAGLORQMSFASIRIGLVDSVKQVYTPPGADNSSLTTRI 120  
 DB 61 VGTGTLTMTWRTGSPSPYNGLVAGLORQMSFASIRIGLVDSVKQVYTPPGADNSSLTTRI 120  
 QY 121 LAGCTGGAAMVTAQOPTDVVKRFPQASIHGSPSRSDRKYSGTMDAYRTIAREGVGLWK 180  
 DB 121 LAGCTGGAAMVTAQOPTDVVKRFPQASIHGSPSRSDRKYSGTMDAYRTIAREGVGLWK 180  
 QY 181 GTLPNIRNAIIVNCAEVVTDILKEKLLDYHLLTDNPFCHVSAFGAGFCATVVASPDV 240

DB 181 GTLPNIRNAIIVNCAEVVTDILKEKLLDYHLLTDNPFCHVSAFGAGFCATVVASPDV 240  
 QY 241 VKTRYNNSPPGOYFSPDLCMKVNAQEGPTAFYKGFPSFRLSGMVMVETYEQLRRA 300  
 DB 241 VKTRYNNSPPGOYFSPDLCMKVNAQEGPTAFYKGFPSFRLSGMVMVETYEQLRRA 300  
 QY 301 LMKVQMLRESPE 312  
 DB 301 LMKVQMLRESPE 312  
 RESULT 6  
 ID AAY54600 standard; protein; 312 AA.  
 XX AAY54600;  
 XX 25-APR-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human uncoupling protein designated HHFCW60.  
 XX  
 KM Human; HHFCW60; mitochondrial uncoupling protein family; muscle wasting;  
 KM uncoupling protein; wound; tissue repair; inflammation; cachexia.  
 XX Homo sapiens.  
 OS  
 XX  
 PN W0200002577-A1.  
 XX  
 PD 20-JAN-2000.  
 PD  
 PF 02-DEC-1998; 98WO-EP007802.  
 XX  
 PR 09-JUL-1998; 98GB-00014926.  
 XX  
 PA (SMITK ) SMITKLINE BECCAM PLC.  
 XX  
 PI Clapham JC, Beeley LJ, Godden RJ;  
 XX  
 DR WPI; 2000-147542/13.  
 DR N-PSDB; AA246055.  
 XX  
 PT Use of uncoupling protein, polynucleotide and compound activating it, in  
 PT treating wounds, inflammation, tissue repair, muscle wasting, and  
 PT cachexia.  
 XX  
 PS Claim 5; Page 22-23; 29pp; English.  
 XX  
 XX The present sequence represents a HHFCW60 polypeptide, which is a member  
 CC of the mitochondrial uncoupling protein family. The HHFCW60  
 CC polynucleotide has homology with human uncoupling protein 2. The  
 CC polynucleotide sequence was isolated from a cDNA library derived from  
 CC human skeletal muscle cell mRNA, and mRNA from the cell lines  
 CC rhadoblastoma, caaki, and SHSY 5Y. The protein is useful in producing  
 CC antibodies and in screening for antagonist and agonist. The  
 CC polynucleotide is useful as a reagent for diagnosis and determining  
 CC susceptibility to the disease by detecting the mutation in the HHFCW60  
 CC gene. The polynucleotide, protein, and antibodies against HHFCW60 are  
 CC useful in screening for the compounds that have an effect on the  
 CC production of mRNA and polypeptides in the cell. These compounds are used  
 CC to treat wounds, tissue repair, inflammation, muscle wasting or cachexia  
 XX  
 SO Sequence 312 AA;  
 Query Match 100.0%; Score 1620; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MWGLKSDVPTMAVFLAGTAACFADLVTPPLDTAKRLQIQENQAVQTARLVQYRG 60  
 DB 1 MWGLKSDVPTMAVFLAGTAACFADLVTPPLDTAKRLQIQENQAVQTARLVQYRG 60  
 QY 61 VGTGTLTMTWRTGSPSPYNGLVAGLORQMSFASIRIGLVDSVKQVYTPPGADNSSLTTRI 120

Db 61 VLGCTIITMVRTEBPCSPYNGLVAGLORQMSFASIRIGLYDSVKQVYTPKGADNSLTTRI 120  
 QY 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRDKTSGTMDARTIAREBGVGLMK 180  
 Db 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRDKTSGTMDARTIAREBGVGLMK 180  
 QY 181 GTLPNIMRNAIVNCAEVVTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPVDV 240  
 Db 181 GTLPNIMRNAIVNCAEVVTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPVDV 240  
 QY 241 VKTRYNNSPPGOYFSPDLCKIKVVAOEGPTAFYKGTPTSPFLRSGSNVVMFVTEYEQKRA 300  
 Db 241 VKTRYNNSPPGOYFSPDLCKIKVVAOEGPTAFYKGTPTSPFLRSGSNVVMFVTEYEQKRA 300  
 QY 301 LMKVQMLRESPP 312  
 Db 301 LMKVQMLRESPP 312

RESULT 7  
 AAY44253  
 ID AAY44253 standard; protein; 312 AA.

XX AAY44253;  
 DT 28-FEB-2000 (first entry)  
 DE Human mitochondrial anion carrier, uncoupling protein-3.  
 XX Mitochondrial uncoupling protein-3; UCP-3; mitochondrial anion carrier;  
 KM MAC; modulator; transport protein; fatty acid anion; mitochondria;  
 KM assay vesicle; metabolic disorder; diabetes; obesity; cancer; human.  
 XX Homo sapiens.  
 OS WO964458-A1.  
 XX 16-DEC-1999.  
 PD 08-JUN-1999; 99WO-US012623.  
 XX 08-JUN-1998; 98US-00093662.  
 PR (UYBO-) UNITV BOSTON.  
 PA Corkey BE, Hamilton JA, Pilch PF, Farmer SR, Kirkland JL;  
 XX WPI; 2000-087200/07.  
 DR N-PSDB; AA229245.  
 PT Identifying modulators of mitochondrial anion carriers, potentially  
 PT useful for treating metabolic disease, e.g. diabetes and obesity.  
 PS Claim 11; Page 73-74; 80pp; English.

XX The present sequence is a human uncoupling protein-3 (UCP-3) which is a  
 CC mitochondrial anion carrier (MAC). The UCPs transport free fatty acid  
 CC anions across the inner mitochondrial membrane to induce cyclical proton  
 CC movement. This transport is tightly related to oxidation of fatty acids  
 CC in the mitochondria, thereby converting fatty acids into energy rather  
 CC than storing them. The uncoupling protein is used in the preparation of  
 CC assay vesicles that are used to identify modulators of MAC activity. MAC  
 CC modulators are useful for treating metabolic disorders, particularly  
 CC diabetes and obesity. Modulators that act as inhibitors can be used to  
 CC treat conditions requiring a reduction in energy expenditure, e.g. in  
 CC cancer patients or the elderly

XX Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2,2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLKPSDVPPTMAVFEFLAGTAACPADLVTEPLDTAKVRLQIQENQAVQTARLVQYRG 60  
 Db 1 MGLKPSDVPPTMAVFEFLAGTAACPADLVTEPLDTAKVRLQIQENQAVQTARLVQYRG 60  
 QY 61 VLGCTIITMVRTEBPCSPYNGLVAGLORQMSFASIRIGLYDSVKQVYTPKGADNSLTTRI 120  
 Db 61 VLGCTIITMVRTEBPCSPYNGLVAGLORQMSFASIRIGLYDSVKQVYTPKGADNSLTTRI 120  
 QY 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRDKTSGTMDARTIAREBGVGLMK 180  
 Db 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRDKTSGTMDARTIAREBGVGLMK 180  
 QY 181 GTLPNIMRNAIVNCAEVVTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPVDV 240  
 Db 181 GTLPNIMRNAIVNCAEVVTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPVDV 240  
 QY 241 VKTRYNNSPPGOYFSPDLCKIKVVAOEGPTAFYKGTPTSPFLRSGSNVVMFVTEYEQKRA 300  
 Db 241 VKTRYNNSPPGOYFSPDLCKIKVVAOEGPTAFYKGTPTSPFLRSGSNVVMFVTEYEQKRA 300  
 QY 301 LMKVQMLRESPP 312  
 Db 301 LMKVQMLRESPP 312

RESULT 8  
 AAB74296  
 ID AAB74296 standard; protein; 312 AA.

XX AAB74296;  
 DT 21-JUN-2001 (first entry)  
 DE Human UCP3 protein.  
 XX UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus.  
 OS Homo sapiens.  
 XX WO200118232-A2.  
 PD 15-MAR-2001.  
 XX 08-SEP-2000; 2000MO-US024784.  
 PR (GENA-) GENAISSANCE PHARM INC.  
 XX (STEP/) STEPHENS J C.  
 PA Chew A, Choi JY, Denton RR, Nandabalan K;  
 XX WPI; 2001-218562/22.  
 PT Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton  
 PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,  
 PT useful for the design of drugs for treating obesity.

XX Claim 10; Fig 6; 94pp; English.  
 CC The present invention relates to the human uncoupling protein 3  
 CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The  
 CC polymorphisms are associated with obesity, especially diabetes mellitus  
 CC associated obesity. They polymorphisms may be identified and analysed to  
 CC determine whether an individual is susceptible to obesity and may be used  
 CC as the basis for targeted design of drugs to treat obesity. The present  
 CC sequence is UCP3 protein

XX Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 4; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2,2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





CC sequence facilitating the expression of the polypeptide. The transgenic  
 CC rodent is useful for determining the phenotypic effect of a compound,  
 CC which may be used for treating UCP3-related disease such as obesity,  
 CC diabetes, hyperlipidemia, body weight disorders, wound healing, cachexia,  
 CC inflammation and tissue repair of atherosclerosis. The transgenic mice  
 CC expressing human UCP3 have significantly reduced body weight compared to  
 CC age-matched wild-type controls despite showing increased food intake,  
 CC and thus are suitable for studies of body weight disorders, diabetes,  
 CC obesity and inflammation and the evaluation of compounds that have  
 CC potential to treat such diseases and disorders. The transgenic rodents  
 CC are also useful for validation of the polypeptide expressed from the  
 CC transgene as a drug target in addition to elucidating the function of a  
 CC gene of interest. The transgenic rodents can also be used to test the  
 CC efficacy of drug and drug administration regime for treating the above  
 CC mentioned disorders and to investigate the effects of various drug  
 CC treatments on the course of the disease

XX Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 4; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2, 2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIGENQAVQTALVQYRG 60  
 DB 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIGENQAVQTALVQYRG 60  
 QY 61 VLGTLLTMVTEGPGSPYNGLVAGLQROMSPASIRIGLYSVQVYTPKADNSLTTRI 120  
 DB 61 VLGTLLTMVTEGPGSPYNGLVAGLQROMSPASIRIGLYSVQVYTPKADNSLTTRI 120  
 QY 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRDKYSGTMDAYRTIAREBVGRLMK 180  
 DB 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRDKYSGTMDAYRTIAREBVGRLMK 180  
 QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDNPFCHFVSAFGAGFCATVVASPDV 240  
 DB 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDNPFCHFVSAFGAGFCATVVASPDV 240  
 QY 241 VKTRYNMSPGQYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300  
 DB 241 VKTRYNMSPGQYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300  
 QY 301 LMKVQMLRESPP 312  
 DB 301 LMKVQMLRESPP 312

RESULT 11  
 ABB81610  
 ID ABB81610 standard; protein; 312 AA.

XX ABB81610;

XX 20-SEP-2002 (first entry)

XX UCP3L protein sequence.

XX UCP3L, UCP3s, diabetes, obesity, diabetic related condition, GKR;  
 XX gene therapy, antidiabetic, anorectic, cardiant, nephrotropic; GK;  
 XX antilipemic; blood glucose; glucokinase regulatory protein, liver;  
 XX glucokinase; hepatic triglyceride accumulation; fibrinogen; HDL;  
 XX hepatic fatty acid oxidation; high density lipoprotein; cholesterol;  
 XX glucose; gestational diabetes; hyperglycaemic related disorder;  
 XX kidney related disorder; cardiovascular disorder.

XX Unidentified.

XX US2002065239-A1.

XX 30-MAY-2002.

XX 14-MAR-2001; 2001US-00808457.

XX 15-MAR-2000; 2000US-0266328P.

XX (CAPL/) CAPLAN S L.  
 XX (BOET) BOETTCHER B R.  
 XX (SLOS/) SLOSBERG E D.  
 XX (CONN/) CONNELLY S.  
 XX (FALE/) KALEKO M.  
 XX (DESA/) DESAI U J.

XX Caplan SL, Boettcher BR, Slosberg ED, Connelly S, Kaleko M;  
 XX Desai UJ;  
 XX WPI, 2002-556735/59.  
 XX N-PSDB; ABQ72999.

PT Treating condition related to elevated blood glucose levels, especially  
 PT diabetes or obesity, involves administering polynucleotide sequence  
 PT encoding glucokinase regulatory protein, to a subject.

XX Disclosure; Page 16-17; 42pp; English.

CC The present invention describes a method (M1) for treating a condition  
 CC related to elevated blood glucose levels, which involves administering a  
 CC polynucleotide sequence encoding a glucokinase regulatory protein (GKR),  
 CC to a subject. Also described: (1) increasing liver glucokinase (GK)  
 CC activity, by administering a polynucleotide sequence encoding GKR; and  
 CC (2) a method (M2) treating diabetes or diabetes-related condition, by  
 CC administering to a subject, one or more metabolism modifying proteins and  
 CC peptides in combination with GK or GKR, or their combination (M1) and  
 CC (M2) can be used for treating diabetes (type I and II diabetes) or  
 CC diabetes-related conditions such as obesity, increased hepatic  
 CC triglyceride accumulation, reduced hepatic fatty acid oxidation,  
 CC increased fibrinogen levels, decreased apo A-I levels, decreased high  
 CC density lipoprotein (HDL) cholesterol levels and decreased hepatic  
 CC glucose utilization. The methods are also useful for treating gestational  
 CC diabetes, hyperglycaemic related disorders such as increased cholesterol,  
 CC kidney related disorders and cardiovascular disorders. The methods  
 CC overcome a limitation to the over-expression of GK in the liver which  
 CC usually increases liver size and hepatic fat accumulation in normal and  
 CC diabetic mice. The present sequence represents a UCP3L protein which is  
 CC given in the exemplification of the present invention

XX Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 5; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2, 2e-165;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIGENQAVQTALVQYRG 60  
 DB 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIGENQAVQTALVQYRG 60  
 QY 61 VLGTLLTMVTEGPGSPYNGLVAGLQROMSPASIRIGLYSVQVYTPKADNSLTTRI 120  
 DB 61 VLGTLLTMVTEGPGSPYNGLVAGLQROMSPASIRIGLYSVQVYTPKADNSLTTRI 120  
 QY 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRDKYSGTMDAYRTIAREBVGRLMK 180  
 DB 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRDKYSGTMDAYRTIAREBVGRLMK 180  
 QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDNPFCHFVSAFGAGFCATVVASPDV 240  
 DB 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDNPFCHFVSAFGAGFCATVVASPDV 240  
 QY 241 VKTRYNMSPGQYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300  
 DB 241 VKTRYNMSPGQYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300  
 QY 301 LMKVQMLRESPP 312  
 DB 301 LMKVQMLRESPP 312

RESULT 12  
ID AAE19348 standard; protein; 312 AA.  
XX  
AC AAE19348;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Human mitochondrial uncoupling protein 3 (UCP3).  
XX  
KW Human; mitochondrial uncoupling protein 3; UCP3; obesity; diabetes;  
XX body weight disorder; gene therapy; chromosome 11q13.  
XX  
OS Homo sapiens.  
XX  
PN WO200207754-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 25-JUL-2001; 2001WO-GE003341.  
XX  
PR 25-JUL-2000; 2000GB-00018248.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Clapham J;  
XX  
DR WPI; 2002-217023/27.  
XX  
DR N-PSDB; AAD30499.  
XX  
PT Use of mitochondrial uncoupling protein 3 polypeptide, polynucleotide and  
XX compounds which activate the polypeptide or polynucleotide for treating  
XX obesity, diabetes or body weight disorder.  
XX  
PS Claim 5; Page 18; 22pp; English.  
XX  
CC The present sequence is human mitochondrial uncoupling protein 3 (UCP3).  
XX The UCP3 gene is located on chromosome 11q13. UCP3 sequences are used for  
XX identifying compounds which modulate their activity. They are used for  
XX the manufacture of a medicament for treating obesity, diabetes and body  
XX weight disorder. UCP3 sequences are also used in gene therapy  
XX  
SQ Sequence 312 AA;  
Query Match 100.0%; Score 1620; DB 5; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVLGKSDVPPPTMAVVKLGGTAACFPADLTTPPLDTAKKRLQIGENQAVQTARLVQYRG 60  
DB 1 MVLGKSDVPPPTMAVVKLGGTAACFPADLTTPPLDTAKKRLQIGENQAVQTARLVQYRG 60  
QY 61 VLGTLTMTVTEGCPSPYNGVAGLQROMSFASIRIGLYDSVKQVTPPKGADNSSLTTRI 120  
DB 61 VLGTLTMTVTEGCPSPYNGVAGLQROMSFASIRIGLYDSVKQVTPPKGADNSSLTTRI 120  
QY 121 LAGCTTGAAVTCAGPTDVVKVRPOASIHGSPSSDRKYSGTMDAYTITAREEGVRLMK 180  
DB 121 LAGCTTGAAVTCAGPTDVVKVRPOASIHGSPSSDRKYSGTMDAYTITAREEGVRLMK 180  
QY 181 GTLPNIRNAINVCAEVYTTDLKEKLDLHLLTDNPFCHVSAFGAGFCATVVASPVDV 240  
DB 181 GTLPNIRNAINVCAEVYTTDLKEKLDLHLLTDNPFCHVSAFGAGFCATVVASPVDV 240  
QY 241 VKTRVNSPPGOVSPDLCMIKWAQSGPTAFYKGFPSFLRLGSNNVWVFVTEQLKRA 300  
DB 241 VKTRVNSPPGOVSPDLCMIKWAQSGPTAFYKGFPSFLRLGSNNVWVFVTEQLKRA 300  
QY 301 LMKVQMLRESPP 312  
DB 301 LMKVQMLRESPP 312

RESULT 13  
ID ADE54391 standard; protein; 312 AA.  
XX  
AC ADE54391;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P55916, SEQ ID NO 194.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
XX spinal segmental nerve injury; chronic constriction injury; CCI;  
XX spared nerve injury; SNJ; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
XX  
PR 01-NOV-2001; 2001US-0346382P.  
XX  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GENO ) GEN HOSPITAL CORP.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'ureo D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
XX  
DR GENBANK; P55916.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX injury (CCI) and spared nerve injury (SNJ)) in an animal (e.g. gene  
XX therapy). The sequence presented is a human protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:  
XX the sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
SQ Sequence 312 AA;  
Query Match 100.0%; Score 1620; DB 7; Length 312;  
Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 DB 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 QY 61 VLGITLTMVTRTEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPPKGADNSLITRI 120  
 DB 61 VLGITLTMVTRTEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPPKGADNSLITRI 120  
 QY 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHLSGSRSDRKYSCTMDAYRTIAREBGVGLWK 180  
 DB 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHLSGSRSDRKYSCTMDAYRTIAREBGVGLWK 180  
 QY 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAGAGFCATVVASPVUV 240  
 DB 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAGAGFCATVVASPVUV 240  
 QY 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGFPSFLRLGSMNVVMFVYTBQLKRA 300  
 DB 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGFPSFLRLGSMNVVMFVYTBQLKRA 300  
 QY 301 LMKVQMLRESPE 312  
 DB 301 LMKVQMLRESPE 312

## RESULT 14

AAW81587  
 ID AAW81587 standard; protein, 312 AA.

AAW81587;  
 AC AAW81587;  
 XX AAW81587;  
 DT 09-FEB-1999 (first entry)

DE Human uncoupling protein 3 (UCP3).  
 XX  
 XX  
 XX

Uncoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;  
 protein catabolism; anti-obesity; inhibitor; muscle wasting; infection;  
 HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;  
 non-insulin dependent diabetes mellitus; diagnosis; human.

OS Homo sapiens.  
 XX  
 XX  
 XX

PN W09845438-A1.  
 XX  
 XX  
 XX

PD 15-OCT-1998.  
 XX  
 XX  
 XX

PF 08-APR-1998; 98WO-US006959.  
 XX  
 XX  
 XX

PR 09-APR-1997; 97US-0043447P.  
 XX  
 XX  
 XX

PR 12-MAY-1997; 97US-0046254P.  
 XX  
 XX  
 XX

PR 15-JUL-1997; 97US-00892745.  
 XX  
 XX  
 XX

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PI Lowell BB, Flier JS;  
 XX  
 XX  
 XX

DR WPI, 1998-594483/50.  
 XX  
 XX  
 XX

DR N-PSDB; AAV71710.  
 XX  
 XX  
 XX

PT New isolated uncoupling protein, UCP-3 - used to develop products for  
 PT modulating thermogenesis in tissues, e.g. for treating obesity or muscle  
 PT wasting caused by infection or cancer.

PS Claim 5; Fig 1A-C; 98PP; English.  
 XX  
 XX  
 XX

CC This represents a human uncoupling protein 3 (UCP3). A host cell  
 CC transformed with a construct comprising the UCP3 nucleic acid can be used  
 CC for the recombinant production of the protein. The UCP3 is involved in  
 CC the regulation of thermogenesis in mammals. The nucleic acids (AAV71710  
 CC to AAV71712) can be used for identifying compounds which alter UCP3  
 CC activity. Enhancers of UCP3 can be used for enhancing protein catabolism  
 CC in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can

CC be used for inhibiting protein catabolism in a mammal such as inhibiting  
 CC muscle wasting. They can be used for curtailing muscle wasting due to  
 CC infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g.  
 CC muscular dystrophy) or as a possible treatment for non-insulin dependent  
 CC diabetes mellitus. The products can also be used for detection and  
 CC diagnosis  
 XX  
 XX  
 SQ Sequence 312 AA;

Query Match 99.8%; Score 1616; DB 2; Length 312;  
 Best Local Similarity 99.7%; Pred. No. 5.9e-165;  
 Matches 311; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 DB 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 QY 61 VLGITLTMVTRTEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPPKGADNSLITRI 120  
 DB 61 VLGITLTMVTRTEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPPKGADNSLITRI 120  
 QY 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHLSGSRSDRKYSCTMDAYRTIAREBGVGLWK 180  
 DB 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHLSGSRSDRKYSCTMDAYRTIAREBGVGLWK 180  
 QY 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAGAGFCATVVASPVUV 240  
 DB 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAGAGFCATVVASPVUV 240  
 QY 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGFPSFLRLGSMNVVMFVYTBQLKRA 300  
 DB 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGFPSFLRLGSMNVVMFVYTBQLKRA 300  
 QY 301 LMKVQMLRESPE 312  
 DB 301 LMKVQMLRESPE 312

## RESULT 15

AAW81588  
 ID AAW81588 standard; protein, 403 AA.

AAW81588;  
 AC AAW81588;  
 XX AAW81588;  
 DT 09-FEB-1999 (first entry)

DE Protein encoded by human UCP3 gene reading frame 1.  
 XX  
 XX  
 XX

XX Uncoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;  
 XX protein catabolism; anti-obesity; inhibitor; muscle wasting; infection;  
 XX HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;  
 XX non-insulin dependent diabetes mellitus; diagnosis; human.

OS Homo sapiens.  
 XX  
 XX  
 XX

PN W09845438-A1.  
 XX  
 XX  
 XX

PD 15-OCT-1998.  
 XX  
 XX  
 XX

PF 08-APR-1998; 98WO-US006959.  
 XX  
 XX  
 XX

PR 09-APR-1997; 97US-0043447P.  
 XX  
 XX  
 XX

PR 12-MAY-1997; 97US-0046254P.  
 XX  
 XX  
 XX

PR 15-JUL-1997; 97US-00892745.  
 XX  
 XX  
 XX

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PI Lowell BB, Flier JS;  
 XX  
 XX  
 XX

DR W09845438-A1.  
 XX  
 XX  
 XX

DR 15-OCT-1998.  
 XX  
 XX  
 XX

PF 08-APR-1998; 98WO-US006959.  
 XX  
 XX  
 XX

PR 09-APR-1997; 97US-0043447P.  
 XX  
 XX  
 XX

PR 12-MAY-1997; 97US-0046254P.  
 XX  
 XX  
 XX

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PI Lowell BB, Flier JS;  
 XX  
 XX  
 XX

Location/Qualifiers  
 1. 403  
 /note= "the encoding reading frame has internal stop  
 codons which are not indicated in this protein"

XX MPI, 1998-594483/50.  
DR N-PSDB; AAV71710.

XX New isolated uncoupling protein, UCP-3 - used to develop products for  
PT modulating thermogenesis in tissues, e.g. for treating obesity or muscle  
PT wasting caused by infection or cancer.

XX Disclosure; Fig 1A-C; 98pp; English.

XX Sequences AAW81588 to AAW81590 represent protein fragments encoded by the  
CC three reading frames of the human uncoupling protein 3 (UCP3) gene. The  
CC invention provides human and mouse UCP3 genes (AAV71710 and AAV71712)  
CC encoding UCP3 proteins (AAW81587 and AAW81595) respectively. A host cell  
CC transformed with a construct comprising the UCP3 nucleic acid can be used  
CC for the recombinant production of the protein. The UCP3 is involved in  
CC the regulation of thermogenesis in mammals. The nucleic acids (AAV71710  
CC to AAV71712) can be used for identifying compounds which alter UCP3  
CC activity. Enhancers of UCP3 can be used for enhancing protein catabolism  
CC in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can  
CC be used for inhibiting protein catabolism in a mammal such as inhibiting  
CC muscle wasting. They can be used for curtailing muscle wasting due to  
CC infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g.  
CC muscular dystrophy) or as a possible treatment for non-insulin dependent  
CC diabetes mellitus. The products can also be used for detection and  
CC diagnosis

XX SQ Sequence 403 AA;

Query Match 99.4%; Score 1610; DB 2; Length 403;

Best Local Similarity 99.4%; Pred. No. 3, 8e-164;

Matches 310; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWGLKPSDVPPTMAVKFLGAGTACPADLVTFFPLDTAKYRLQIQENQAVQTARLVQYRG 60  
DB 60 MWGLKPSDVPPTMAVKFLGAGTACPADLVTFFPLDTAKYRLQIQENQAVQTARLVQYRG 119  
QY 61 VLGTLTWRTREGSPYNGVAGLOROMSFASIRIGLYDSVKQVYTPKGNSSLTTRI 120  
DB 120 VLGTLTWRTREGSPYNGVAGLOROMSFASIRIGLYDSVKQVYTPKGNSSLTTRI 179  
QY 121 IAGCTTGAMAATVCAOPTDVVKVRFQASIHGSPRSRDKYSGTMDAYRTIAREEGVGLMK 180  
DB 180 IAGCTTGAMAATVCAOPTDVVKVRFQASIHGSPRSRDKYSGTMDAYRTIAREEGVGLMK 239  
QY 181 GTLPNIMRNNAIVNCAEVVYDILKEKLDYHLTLTNFCHVYSAFGAGFCATVVASPDV 240  
DB 240 GTLPNIMRNNAIVNCAEVVYDILKEKLDYHLTLTNFCHVYSAFGAGFCATVVASPDV 299  
QY 241 VETRTMNSPQGYFSPPLDMIMVQAEQGTAFYKGFPSFLRIGSMNVMPFTYEOLKRA 300  
DB 300 VETRTMNSPQGYFSPPLDMIMVQAEQGTAFYKGFPSFLRIGSMNVMPFTYEOLKRA 359  
QY 301 LMKVOMLRESPP 312  
DB 360 LMKVOMLRESPP 371

Search completed: May 17, 2004, 11:51:55  
Job time : 61 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: May 17, 2004, 11:49:46 ; Search time 20 Seconds  
(without alignments)  
1500.588 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620  
Sequence: 1 MVLKPSDVPPTMAVKFLGA.....TYEQLKALMKVQLRESPP 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	100.0	312	2 JCS522	uncoupling protein
2	910.5	56.2	307	2 G01858	uncoupling protein
3	905	55.9	306	2 A32446	uncoupling protein
4	903.5	55.8	307	2 A26294	uncoupling protein
5	885.5	54.7	306	2 A31106	mitochondrial unco
6	873.5	53.9	307	2 S34268	uncoupling protein
7	846	52.2	288	2 S03603	uncoupling protein
8	687	42.4	306	2 T07293	uncoupling protein
9	682	42.1	306	2 T47570	uncoupling protein
10	673	41.5	306	2 T52024	uncoupling protein
11	524	32.3	325	2 JC7553	brain mitochondria
12	500.5	30.9	313	2 T05577	uncoupling protein
13	478.5	29.5	305	2 H86274	F7A19.22 protein -
14	472.5	29.2	313	2 D84613	hypothetical prote
15	439	27.1	343	2 T15253	hypothetical prote
16	432	26.7	314	2 A36305	2-oxoglutarate/mal
17	427	26.4	323	2 T25459	hypothetical prote
18	426	26.3	314	2 A56650	2-oxoglutarate car
19	385.5	23.9	282	2 T49628	probable dicarboxy
20	373	23.0	280	2 S44091	oxoglutarate/malat
21	364.5	22.5	298	2 S51351	hypothetical prote
22	327.5	20.2	324	2 S25357	mitochondrial unco
23	318	19.6	302	2 S65040	2-oxoglutarate/mal
24	310	19.1	297	2 T07405	oxoglutarate/malat
25	309	18.5	302	2 S65042	oxoglutarate/mal
26	299.5	18.5	331	2 T51899	probable 2-oxoglut
27	293	17.9	322	2 S57116	probable carrier p
28	289.5	17.1	320	2 T37603	probable oxalacet
29	272.5	16.8	311	2 A46595	tricarboxylate tra

30	268	16.5	93	2 S16082	uncoupling protein
31	267.5	16.5	309	2 T48156	hypothetical prote
32	267	16.5	298	2 B43646	ADP,ATP carrier pr
33	265	16.4	298	1 S03894	ADP,ATP carrier pr
34	258	15.9	298	1 XWBO	ADP,ATP carrier pr
35	258	15.9	358	2 T09109	envelope protein l
36	257	15.9	298	2 S37210	ADP,ATP carrier pr
37	256.5	15.8	373	2 S48451	probable membrane
38	253.5	15.6	311	2 G01789	citrate transpor
39	252.5	15.6	339	2 A41677	ADP,ATP carrier pr
40	252	15.6	298	2 T60173	adenine nucleotide
41	252	15.6	355	2 T09110	envelope protein l
42	251	15.5	301	2 S51132	ADP,ATP carrier pr
43	250	15.4	298	2 S31814	ADP,ATP carrier pr
44	249.5	15.4	318	1 A31978	ADP,ATP carrier pr
45	249	15.4	352	2 T01729	mitochondrial solu

ALIGNMENTS

RESULT 1

JCS522

uncoupling protein UCP3, mitochondrial - human

C/Species: Homo sapiens (man)

C/Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 21-Jan-2000

C/Accession: JCS522

R/Vidal-Puig, A.; Solanes, G.; GrunJC, D.; Flier, J.S.; Lowell, B.B.

Biochem. Biophys. Res. Commun. 235, 79-82, 1997

A/Title: UCP3: An uncoupling protein homologue expressed preferentially and abundantly i

A/Reference number: JCS522; MUID:9739440; PMID:9196039

A/Accession: JCS522

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-312 <VID>

A/Cross-references: DDBJ:AF001787; NID:G2198812; PIDN:ANC51369.1; PID:G2198813

A/Experimental source: skeletal muscle

A/Comment: This protein is an inner mitochondrial membrane transporter which dissipates

A/Genes: GDB:UCP3

A/Cross-references: GDB:6278985

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C/Keywords: mitochondrion

F/10-106/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F/113-207/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F/214-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1620; DB 2; Length 312;

Best Local Similarity 100.0%; Pred. No. 2.6e-14;

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIQENQAVQTRALVQYRG	60
DB	1	MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIQENQAVQTRALVQYRG	60
QY	61	VLGTLITWRTGSPSPYNGVLVAGLQRMSPASIRIGLVDSKYQVYTPKADNSLTTRI	120
DB	61	VLGTLITWRTGSPSPYNGVLVAGLQRMSPASIRIGLVDSKYQVYTPKADNSLTTRI	120
QY	121	LAGCTTGANAATCAQPTDVVKTRFQASIHGSPRSRKSGTMDAYRTIAREGCVGLWK	180
DB	121	LAGCTTGANAATCAQPTDVVKTRFQASIHGSPRSRKSGTMDAYRTIAREGCVGLWK	180
QY	181	GTLPTNMRNALVNCAEVYVDILKEKLLVHLTDNPFCHPVSAFGAGCATVVASPVV	240
DB	181	GTLPTNMRNALVNCAEVYVDILKEKLLVHLTDNPFCHPVSAFGAGCATVVASPVV	240
QY	241	VKTRVNSPPGOYFSPDLDMIKNVAGGPTAFYKGFPSFLRIGSNVNVVFVTEQLKKA	300
DB	241	VKTRVNSPPGOYFSPDLDMIKNVAGGPTAFYKGFPSFLRIGSNVNVVFVTEQLKKA	300
QY	301	LKRVQLRESPP 312	

DB 301 LMKVLMRESPE 312

# RESULT 2

G01858 uncoupling protein 1, mitochondrial - human

N:Alternate names: UCP1

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text\_change 20-Jun-2000

C:Accession: G01858; S78473; S29141; A60793; A45763

R:Bouillaud, F. submitted to the EMBL Data Library, June 1995

A:Reference number: G08642

A:Accession: G01858

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-307 <BOU1>

A:Cross-references: EMBL:U28480; NID:g1155218; PIDN:AAA05271.1; PID:g1155219

A:Accession: S78473

A:Molecule type: DNA

A:Residues: 1-20, 'P', '22-108', 'SK', '111,113-133', 'S', '135-197', 'T', '199-216', 'L', '218-307 <CAS>

A:Cross-references: EMBL:X51952; NID:g37606; PIDN:CAA36214.1

R:Bouillaud, F.; Villarroya, F.; Hentz, E.; Raimbault, S.; Cassard, A.M.; Ricquier, D.

Clin. Sci. 75, 21-27, 1988

A:Title: Detection of brown adipose tissue uncoupling protein mRNA in adult patients by

A:Reference number: A60793; MUID:88311701; PMID:3165741

A:Accession: A60793

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 193-133, 'S', '135-196 <BOU>

C:Comment: This protein is responsible for the generation of heat by brown fat.

C:Genetics:

A:Gene: GDB:UCP1; UCP

A:Cross-references: GDB:126179; OMIM:113730

A:Map position: 4q31-4q31

A:ntons: 42/3; 109/1; 176/1; 210/1; 270/2

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: adipose tissue; duplication; mitochondrion; transmembrane protein

F:10-103/Domain: ADP/ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>

F:209-296/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 56.2%; Score 910.5; DB 2; Length 307;  
Best Local Similarity 58.7%; Pred. No. 5.1e-76;  
Matches 178; Conservative 47; Mismatches 73; Indels 5; Gaps 2;

DB 1 MVLKRSVDPPTMAVFLGAGTACFADLVTPPLDTAKVRLIOGENQAVQARLVQYRG 60  
1 MGLTASDVHPTLGVLFSGALACADVITPPLDTAKVRLIOVQSE--CPTISVIRYKG 57  
DB 1 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 120  
61 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 120  
DB 58 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 117  
117 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 117  
DB 121 LAGCTTGMAVTCAGPTDVVKKRFGASIHGSPRSRDKSGTMDAYRTTAREGVRGLMK 180  
121 LAGCTTGMAVTCAGPTDVVKKRFGASIHGSPRSRDKSGTMDAYRTTAREGVRGLMK 180  
DB 118 LAGLTGGVAVFGQPTLVKKRVLQAQSHLGLKIP--RYTGYNAYRIATTEGLGLMK 175  
118 LAGLTGGVAVFGQPTLVKKRVLQAQSHLGLKIP--RYTGYNAYRIATTEGLGLMK 175  
DB 181 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 240  
181 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 240  
DB 176 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 235  
176 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 235  
DB 241 VKTRVNSPPGQYFSPDLDCMIMKVAQEGPTAFYKGFPSFLRLGSMNVVMFVYEQLKRA 300  
241 VKTRVNSPPGQYFSPDLDCMIMKVAQEGPTAFYKGFPSFLRLGSMNVVMFVYEQLKRA 300  
DB 236 VKTRFINSPPGQYKSPVNCAMKFTNKGPTAFKGLVPSFLRLGSMNVVMFVCFEQLKRB 295  
236 VKTRFINSPPGQYKSPVNCAMKFTNKGPTAFKGLVPSFLRLGSMNVVMFVCFEQLKRB 295

QY 301 LMK 303  
DB 296 LSK 298

## RESULT 3

A22446 uncoupling protein - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 25-Sep-1989 #sequence revision 25-Sep-1989 #text\_change 18-Feb-2000

C:Accession: A22446

R:Balogh, A.G.; Ridley, R.G.; Patel, H.V.; Freeman, K.B.

Biochem. Biophys. Res. Commun. 161, 156-161, 1989

A:Title: Rabbit brown adipose tissue uncoupling protein mRNA: use of only one of two po

A:Reference number: A22446; MUID:89273628; PMID:2730654

A:Accession: A22446

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-306 <BAL>

A:Cross-references: GB:X14696

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: duplication; mitochondrion; transmembrane protein

F:10-103/Domain: ADP/ATP carrier protein repeat homology <ACPI>

F:109-201/Domain: ADP/ATP carrier protein repeat homology <ACPI>

F:208-295/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 55.9%; Score 905; DB 2; Length 306;  
Best Local Similarity 57.8%; Pred. No. 1.6e-75;  
Matches 175; Conservative 49; Mismatches 73; Indels 6; Gaps 3;

DB 1 MVLKRSVDPPTMAVFLGAGTACFADLVTPPLDTAKVRLIOGENQAVQARLVQYRG 60  
1 MGLTASDVHPTLGVLFSGALACADVITPPLDTAKVRLIOVQSE--CPTISVIRYKG 57  
DB 1 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 120  
61 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 120  
DB 58 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 116  
116 VGTITLWRTGSPCPYNGLVAGLQROMSPASIRIGLYDSVQYVTPKGDNSLITRI 116  
DB 121 LAGCTTGMAVTCAGPTDVVKKRFGASIHGSPRSRDKSGTMDAYRTTAREGVRGLMK 180  
121 LAGCTTGMAVTCAGPTDVVKKRFGASIHGSPRSRDKSGTMDAYRTTAREGVRGLMK 180  
DB 117 SAGLTGGVAVFGQPTLVKKRVLQAQSHLGLKIP--RYTGYNAYRIATTEGLGLMK 174  
117 SAGLTGGVAVFGQPTLVKKRVLQAQSHLGLKIP--RYTGYNAYRIATTEGLGLMK 174  
DB 181 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 240  
181 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 240  
DB 175 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 234  
175 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTDPFCHFSAGCATVVASPVVY 234  
DB 241 VKTRVNSPPGQYFSPDLDCMIMKVAQEGPTAFYKGFPSFLRLGSMNVVMFVYEQLKRA 300  
241 VKTRVNSPPGQYFSPDLDCMIMKVAQEGPTAFYKGFPSFLRLGSMNVVMFVYEQLKRA 300  
DB 235 VKTRFINSPPGQYKSPVNCAMKFTNKGPTAFKGLVPSFLRLGSMNVVMFVCFEQLKRB 294  
235 VKTRFINSPPGQYKSPVNCAMKFTNKGPTAFKGLVPSFLRLGSMNVVMFVCFEQLKRB 294  
QY 301 LMK 303  
DB 295 LMR 297

## RESULT 4

A26294 uncoupling protein - rat

N:Alternate names: UCP

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Jul-1987 #sequence revision 22-Jul-1987 #text\_change 18-Feb-2000

C:Accession: A26294; A29278; S03842; A61566

R:Bouillaud, F.; Welschenbach, J.; Ricquier, D.

J. Biol. Chem. 261, 1487-1490, 1986

A:Reference number: A26294; MUID:86111804; PMID:3753702

A:Accession: A26294

A:Molecule type: mRNA

A:Residues: 1-307 <BOU>

A:Cross-references: GB:M1814; NID:g207556; PIDN:AAA19671.1; PID:g207557

R:Ridley, R.G.; Patel, H.V.; Geiger, G.B.; Morton, R.C.; Freeman, K.B.

Nucleic Acids Res. 14, 4025-4035, 1986

A:Title: Complete nucleotide and derived amino acid sequence of cDNA encoding the mitoc





F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F:209-236/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 53.9%; Score 873.5; DB 2; Length 307;

Best Local Similarity 56.8%; Pred. No. 1.3e-72;  
Matches 172; Conservative 45; Mismatches 81; Indels 5; Gaps 2;

```
QY 1 MVGLKPSVPPPTMVKFAGTAACFADLVTPPTDPAKRLQIOGENAVQTARLVQYRG 60
DB 1 MNPPTSTVHTPMGKIRISAGVAAACLAADITPPTDPAKRLQIOGENISST---IRKKG 57
QY 61 VLGTLLMTVTEGSPYNGVLVAGLQIQWSPASIRIGLYDSVKQYTPKGDNSLTTRI 120
DB 58 VLGTITLAKTEGLPKLYSGLPAGIQROISFASLIRIGLYDQVEYFSSGKETPTLGRRI 117
QY 121 LAGCTGMAVTCQOPTVVVKVRPAPASIHGSPSRDRYSGMDVRYRTIAREBGRGLMK 180
DB 118 SAGLMTGVAVFIQPTVEVVKVRLQAQSHHGIRK-RTGTYNAYRLIATTESFTLMK 175
QY 181 GLTPIMENATVNCAEVVTYDLIKEKLDYHLITDNPCHFEVSAPGAFCAVTVASPYDV 240
DB 176 GTTPRLANVINCELVITYDLMKALVNNQIADVDVCHLSAFVAGCTTFLASPADV 235
QY 241 VKTRVNSPPQGYFSPDLDMIRVNAQEGPTAFYKGFPSFLRLGSMNVVMPYTYEQLKRA 300
DB 236 VKTRFINSLPQGYFSPVSCAMTMLTKEGPTAFKGFVPSFLRLASNVIMFVCFEQLKKE 295
QY 301 LMK 303
DB 296 LSK 298
```

## RESULT 7

uncoupling protein - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 20-Jun-2000

C:Accession: S03603; S05075

R:Castella, L.; Bouillaud, F.; Forest, C.; Ricquier, D.

Nucleic Acids Res. 17, 2131, 1989

A:Title: Nucleotide sequence of a cDNA encoding bovine brown fat uncoupling protein. Hom

A:Reference number: S03603; MUID:89183626; PMID:2928121

A:Accession: S03603

A:Molecule type: mRNA

A:Residues: 1-288 <CDS>

A:Cross-references: EMBL:X14064; NID:91495201; PIDN:CAA32227.1; PID:91495202

R:Ricquier, D.

submitted to the EMBL Data Library, January 1989

A:Reference number: S05075

A:Accession: S05075

A:Molecule type: mRNA

A:Residues: 1-195,201, 'T', 203, 'RCC', 204-288 <RIC>

A:Cross-references: EMBL:X14064

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; mitochondrion; transmembrane protein

F:1-87/Domain: ADP,ATP carrier protein repeat homology (fragment) <ACP1>

F:92-184/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:191-277/Domain: ADP,ATP carrier protein repeat homology <ACP3>

## Query Match

Best Local Similarity 52.2%; Score 846; DB 2; Length 288;

Matches 168; Conservative 46; Mismatches 61; Indels 10; Gaps 5;

```
QY 20 AGTAACPADLVTPPTDPAKRLQIOGENAVQTARLVQYRGVLTLLMTVTEGSPSPVN 79
DB 4 AGTAACPADLVTPPTDPAKRLQIOGE---CLISSAIRKGVAGTITLAKTBGVKLYS 60
QY 80 GVAAGLQROMSPASIRIGLYDSVKQYTPKGDNSLTTRIAGCTTGAAVTCQOPTDV 139
DB 61 GTPAGLQROISLASIRIGLYDQVEFTT--GKEASLGSKISGMLTGVAVFIQPTLV 118
QY 140 VVYRFQASVHL-GPSSDRKYSGMTDAYRTIAREBGRGLMKVTLTPNIRNATVNCAEV 198
DB 141 VVYRFQASVHL-GPSSDRKYSGMTDAYRTIAREBGRGLMKVTLTPNIRNATVNCAEV 198
```

DB 119 VKVRLQAQSHLHGK---PRYGTYNAYRLIATTEGLTGMLKGTSPNLTNNVINCHELV 175

QY 199 TYDLIKEKLDYHLITDNPCHFEVSAPGAFCAVTVASPYDVVKTRVNSPPQGYFSPDL 258

DB 176 TYDLMKELVANKLADVDVCHFEVSAPGAFCAVTVASPYDVVKTRFVNSPPQNTSVPN 235

QY 259 CMIRVNAQEGPTAFYKGFPSFLRLGSMNVVMPYTYEQLKRALMK 303

DB 236 CAMMLTRREGSAPFVKGFVPSFLRLGSMN-IMFVCFERLQELMK 279

## RESULT 8

T07793

uncoupling protein (clone StucP7), mitochondrial - potato

C:Species: Solanum tuberosum (potato)

C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000

C:Accession: T07793

R:Latol, W.; Klein, M.; Riemer, J.W.; Mueller-Roeber, B.; Fleury, C.; Bouillaud, F.;

Nature 389, 135-136, 1997

A:Title: A plant cold-induced uncoupling protein.

A:Reference number: Z16136; MUID:97441051; PMID:9296489

A:Accession: T07793

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-306 <LML>

A:Cross-references: EMBL:Y11220; NID:92398828; PIDN:CAA72107.1; PID:92398829

A:Experimental source: cv. Desiree

A:Genome: nuclear

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: mitochondrion

Query Match 42.4%; Score 687; DB 2; Length 306;

Best Local Similarity 47.7%; Pred. No. 1.9e-55;

Matches 146; Conservative 49; Mismatches 101; Indels 10; Gaps 5;

```
QY 7 SDVPTMAVKFLGAGTAACFADLVTPPTDPAKRLQIOGENAVQTARLVQYRGVLTGTL 66
DB 10 SDI--SFAGIFASAFACFAEACTLPDITAKVRLQLOKKAEBGDGLPKYRGLGTVG 67
QY 67 TMVTEGSPYNGVLVAGLQIQWSPASIRIGLYDSVKQYTPKGDNSLTTRIAGCT 125
DB 68 TIAKEGSLASLMKGIPELHRQCYGGIRKQWTEVKNLYGKHVGVPLSKTILALT 127
QY 126 TGAAVTCQOPTDVVKVRFQASVHLGSPSRDRKYSGMTDAYRTIAREBGRGLMKVTL 185
DB 128 TGAAGTITANFTDPAKRLQIOGEKCL-PAGVRRRSGLANAYSTIVKQGVNLTGGLPN 186
QY 186 IMRNAIVNCAEVVTYDLIKEKLDYHLITDNPCHFEVSAPGAFCAVTVASPYDVVKTRY 245
DB 187 IGRNATINAAHLASVDQKAVLRIPGPTDVVVTLLIAGLGAFFAVCIGSPVDVVKSRM 246
QY 246 MNSPPQGYFSPDLDMIRVNAQEGPTAFYKGFPSFLRLGSMNVVMPYTYEQLKRALMKVQ 305
DB 247 MGD--SAKNTLDCVKTLLKNDGFLAFYKGFIPNFGRLGSMNVVMTLLEQAKKVVXSL- 303
QY 306 MLRESP 311
DB 304 ---ESP 306
```

## RESULT 9

T47570

uncoupling protein (imported) - Arabidopsis thaliana

N:Alternate names: protein P24B22.70

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 03-Nov-2000

C:Accession: T47570; T52023

R:Blöcker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Queciet, F.; Salanoubat, M.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23016

A:Accession: T47570

A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-306 <BLO>  
 A:Cross-references: EMBL:AL132957  
 A:Experimental source: cultivar Columbia; BAC clone F24B22  
 Riialoi, M.  
 submitted to the EMBL Data Library, August 1997  
 A:Reference number: Z25905  
 A:Accession: T52023  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-306 <LAL>  
 A:Cross-references: EMBL:AJ001264; PIDN:CAA04638.1  
 C:Genetics:  
 A:Map position: 3  
 A:Intons: 26/3; 98/3; 125/1; 169/3; 202/3; 237/3; 263/3; 292/3  
 A:Note: F4B22.70  
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 42.1%; Score 682; DB 2; Length 306;  
 Best Local Similarity 48.3%; Pred. No. 5.5e-55;  
 Matches 146; Conservative 46; Mismatches 100; Indels 10; Gaps 6;

QY 1 MVLGKPSD--VPPTMVAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVQTAFLVQY 58  
 DB 1 MVAAGSDLSLPKTFAC-----SAFAACVGEVCTIPDTAKVRLQIQ-KSALAGDVTLPKY 55  
 QY 59 RGVLTITLMTVTEGCGSPYNGVLVAGLQRMSPASIRIGLYDSVKQVYTPKG-ADNSSLT 117  
 DB 56 RGLGTGTIAREEGRLSLMKGVVPGIHRQCLFEGGLIGMVEPKNIYVKDIFVGDVPLS 115  
 QY 118 TRLAGCTTGAMAVTCAOPTDVVVFQASIHGSPSRDYSKGTMDAYRTIAREBGVRG 177  
 DB 116 KTLIAGLTGALGIMVNPFDLVKVRLOAEGLA-AGAPRRISGALNASTIYRQEGVRA 174  
 QY 178 LMKGTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNPCHFVSAFGAFCAVVASP 237  
 DB 175 LMTVGLGNVARNAINAAELASDYQVKEITLIKIPGFTDNVTHILSLGAGFPAVCIGSP 234  
 QY 238 VDVVKTRYNMSPGQYFSPDCKIKVNAOEGPFAFYKGFPSFLRLGSNNVWVFVYEQ 297  
 DB 235 VDVVKSRMMDG-SGAYKGTIDCFVKTLKSDGPMAFYKGFIPNFGRLGSNNVWVFVLEQA 293  
 QY 298 KR 299  
 DB 294 KK 295

RESULT 10  
 T52024  
 uncoupling protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 03-Nov-2000  
 C:Accession: T52024  
 R:Maiz, I.G.; Benedetti, C.E.; Leite, A.; Turcinelli, S.R.; Vercesi, A.E.; Arruda, P.  
 FEBS Lett. 429, 403-406, 1998  
 A:Title: AtPUMP: an Arabidopsis gene encoding a plant uncoupling mitochondrial protein.  
 A:Reference number: Z22968; MUID:9662458; PMID:9662458  
 A:Accession: T52024  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-306 <MAI>  
 A:Cross-references: EMBL:AJ223983; PIDN:CAA11757.1  
 C:Genetics:  
 A:Gene: PUMP  
 C:Function:  
 A:Description: may play a role in heat-requiring physiological events  
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 41.5%; Score 673; DB 2; Length 306;

Best Local Similarity 48.0%; Pred. No. 3.7e-54;  
 Matches 145; Conservative 46; Mismatches 101; Indels 10; Gaps 6;  
 QY 1 MVLGKPSD--VPPTMVAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVQTAFLVQY 58

DB 1 MVAAGSDLSLPKTFAC-----SAFAACVGEVCTIPDTAKVRLQIQ-KSALAGDVTLPKY 55  
 QY 59 RGVLTITLMTVTEGCGSPYNGVLVAGLQRMSPASIRIGLYDSVKQVYTPKG-ADNSSLT 117  
 DB 56 RGLGTGTIAREEGRLSLMKGVVPGIHRQCLFEGGLIGMVEPKNIYVKDIFVGDVPLS 115  
 QY 118 TRLAGCTTGAMAVTCAOPTDVVVFQASIHGSPSRDYSKGTMDAYRTIAREBGVRG 177  
 DB 116 KTLIAGLTGALGIMVNPFDLVKVRLOAEGLA-AGAPRRISGALNASTIYRQEGVRA 174  
 QY 178 LMKGTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNPCHFVSAFGAFCAVVASP 237  
 DB 175 LMTVGLGNVARNAINAAELASDYQVKEITLIKIPGFTDNVTHILSLGAGFPAVCIGSP 234  
 QY 238 VDVVKTRYNMSPGQYFSPDCKIKVNAOEGPFAFYKGFPSFLRLGSNNVWVFVYEQ 297  
 DB 235 VDVVKSRMMDG-SGAYKGTIDCFVKTLKSDGPMAFYKGFIPNFGRLGSNNVWVFVLEQA 293  
 QY 298 KR 299  
 DB 294 KK 295

RESULT 11  
 JC7553  
 brain mitochondrial carrier protein-1 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001  
 C:Accession: JC7553  
 R:Mizuno, T.; Miura-Suzuki, T.; Yamaehta, H.; Mori, N.  
 Biochem. Biophys. Res. Commun. 278, 691-697, 2000  
 A:Title: Distinct regulation of brain mitochondrial carrier protein-1 and uncoupling pr  
 A:Reference number: JC7553; MUID: 20549014; PMID:11095970  
 A:Accession: JC7553  
 A:Molecule type: mRNA  
 A:Residues: 1-325 <MTZ>  
 A:Cross-references: GB:AF300424  
 A:Experimental source: strain Male Wistar/SR  
 C:Comment: This protein, a member of mitochondrial uncoupling protein family, has the rc  
 ty to uncouple oxidative phosphorylation in yeast.  
 C:Genetics:  
 A:Gene: bmcpl  
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
 C:Keywords: brain; carrier protein; mitochondrion

Query Match 32.3%; Score 524; DB 2; Length 325;  
 Best Local Similarity 38.8%; Pred. No. 2.1e-40;  
 Matches 112; Conservative 60; Mismatches 101; Indels 16; Gaps 5;

QY 17 FLGAGTACFADLVTPPLDTAKVRLQIQENQAVQTAFLVQYRGVLTITMTVTEGPCS 76  
 DB 44 FVVGGLASIVAEFGTPEVDLTTRLOVQSGSIDVR-FKEIKYGMFALPRIYREEGILA 102  
 QY 77 PNYGLVAGLQRMSPASIRIGLYDSVKQVYTPKGADNSSLTTRLAGCTTGAMAVTCAOP 136  
 DB 103 LYSIGLAPALRKQASYGITIKIGIQLKRLVER-LEDETLIMWIGVSVISSTIANP 161  
 QY 137 TDVVKVRFQASIHGSPSRDYSKGTMDAYRTIAREBGVRGIMKGTLPNIRNAIVNCA 195  
 DB 162 TDVLKIRMQAGSL-----FGSWIGSFIDYQEGRTGLMRGVPTAQRALIVGV 213  
 QY 196 EVVTTDILKEKLDYHLITDNPCHFVSAFGAFCAVVASPVDVVKTRYNMSP----- 250  
 DB 214 ELVPYDITKRLHLSVGLGDTILTHFVSSFTGAGALASNPDVAVTRMNDQRAIVGHV 273  
 QY 251 GQYFSPDCKIKVNAOEGPFAFYKGFPSFLRLGSNNVWVFVYEQ 299  
 DB 274 DLKGTIDGLIKMKHGFALYKGFPMWNLRLGPNMIIFFIYEQDKR 322

RESULT 12  
 T05577



**RESULT 15**

T15253

hypothetical protein K0781.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C:\Data: 20-Sep-1999 #sequence 20-Sep-1999 #text\_change 17-Mar-2000

C;Accession: T15253

R;Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, May 1997.

**A;Description:** The sequence of *C. elegans* cosmid K07B1

A;Reference number: Z18317

A;Accession: T15253

A; Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-343 &lt;PAU&gt;

**A; Cross-references:** EMBL:AF003384; NID:g2088817; PID:K07B11  
**Environmental source:** strain Bristol N2; clone K07B11

A; Experimental source: strain Bristol N2; clone K07B1

C;Genetics:

A;Gene: CESP:K07B1.3

A;Map position: 5

A; Introns: 81/1; 131/3; 236/3; 279/2

c;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match	27.18;	Score 439;	DB 2;	Length 343;
	33.38;	Score 439;	DB 2;	Length 343;

Best Local Similarity 33.3%; Pred. No. 1.5e-32;  
 Matched 00; Corrected 56; Mismatches 118; Indels 22; Gaps 3;

Matches 98; Conservative 56; Mismatches 118; Indels 22; Gaps 3;

22 TACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRGVLGTLTMVTEGPCSPYNGL 81

Db 49 TAA LVAETVTPLDITKRLQIARNKFTKGGIMVQ-----VTYDIIRREGAMALWTGV 102

82 VAGLÖRÖMSFASIRIGLYDSVKÖVYTPKGADNS-SLTTRILAGCTTGAMAVTCAQPTDV 140

Db 103 APAITRHYITYTGIRMGAYEQIRLLTENKEVEKSFPLWKSMLCGAFSGLIAQFAASPTDLV 1622

141 KVRFOASIHGSPSRSDRKYSGTMDAYRTIAREEGVRLWKGTLPNIMRNAIVNCAEVVY 200

Db 163 KVOMMEGLBRLQKOPRLRYTGATDCFRSLYRTQGEFGLWIGMMPNCORALLNMADIATY 2222

201 DTI:KKKI.I.DYHI.L.TDNEPCHVSAFGAGECATVVASPVDVKTRYM----- 246

333 PSYHCHI TDNEFI KDNWI THAVBSACAGI.AAATVSI.PSDVNTKTPMDOIPHEI.DAKMMHK 282

247 WOODCOCKEYNT DOWTMA/AFCTTA FVZCETHOAEY DI CAGTHTMMEVEOI YB 200

[illegible]

Search completed: May 17, 2004, 11:53:55

Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:49:15 ; Search time 45 Seconds  
(without alignments)  
2187.593 Million cell updates/sec

Title: US-09-423-410-4  
Perfect score: 1620  
Sequence: 1 MWGLKPSDVPPTMAVKFLGA.....TYEQKRALMKYQMLRESPEF 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP yvirus:\*  
16: SP bacteriaph:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1370	84.6	312	11 Q7TNY4	Q7TNY4 dicostonyx
2	1350	83.3	299	11 Q9ER16	Q9ER16 phodopus su
3	1178	72.7	310	6 Q7YR13	Q7YR13 antechinus
4	1173.5	72.0	307	13 Q7ZXN1	Q7ZXN1 xenopus lae
5	1166.5	72.4	307	13 Q90X50	Q90X50 melalegris g
6	1163.5	71.8	309	11 Q9R246	Q9R246 mus musculus
7	1162.5	71.8	307	13 Q9DDT7	Q9DDT7 gallus gall
8	1159.5	71.6	307	13 Q8AYM4	Q8AYM4 gallus gall
9	1159.5	71.6	309	11 Q8CBU0	Q8CBU0 mus musculus
10	1158.5	71.5	309	11 Q9ER17	Q9ER17 phodopus su
11	1141	70.4	304	13 Q9ER90	Q9ER90 eupetomena
12	1127.5	69.6	309	13 Q7ZVP4	Q7ZVP4 brachydanto
13	1026	63.3	274	6 Q7YR12	Q7YR12 emmihopis
14	1004.5	62.0	273	6 Q9XSE1	Q9XSE1 bos taurus
15	929	57.3	193	6 Q9NID8	Q9NID8 macaca mula
16	925.5	57.1	309	6 Q9GMZ1	Q9GMZ1 canis fami1

17	879.5	54.3	307	11 Q9ER18	Q9ER18 phodopus su
18	866.5	53.5	307	11 Q8K404	Q8K404 dicostonyx
19	834.5	51.5	224	13 Q8QG96	Q8QG96 pagrus majo
20	781.5	48.2	209	13 Q7T3C5	Q7T3C5 brachydanto
21	713.5	44.0	304	10 Q8LNZ1	Q8LNZ1 heliodicer
22	687	42.4	306	10 Q24391	Q24391 solanum tub
23	687	42.4	306	10 Q8SA58	Q8SA58 lycopersico
24	684.5	42.3	300	10 Q9AVG1	Q9AVG1 oryza sativ
25	682	42.1	306	10 Q81845	Q81845 arabidopsis
26	681.5	42.1	310	10 Q8S4C4	Q8S4C4 zea mays (m
27	675.5	41.7	303	10 Q9MBE7	Q9MBE7 sympllocarpu
28	673	41.5	306	10 Q65623	Q65623 arabidopsis
29	639	39.4	305	10 Q9ZWG1	Q9ZWG1 arabidopsis
30	619.5	38.2	293	10 Q9AVG2	Q9AVG2 oryza sativ
31	615	38.0	286	10 Q9FX05	Q9FX05 triticum ae
32	606	37.4	286	10 Q9FX06	Q9FX06 triticum ae
33	592	36.5	268	10 Q9MBE6	Q9MBE6 sympllocarpu
34	545	33.6	154	6 Q9NID9	Q9NID9 macaca mula
35	541	33.4	242	10 Q94F06	Q94F06 mangifera 1
36	538	33.2	241	10 Q8W1A4	Q8W1A4 glycine max
37	537	33.1	241	10 Q8W1A3	Q8W1A3 glycine max
38	524	32.3	322	11 Q9JMH0	Q9JMH0 rattus norv
39	524	32.3	325	11 Q9EP88	Q9EP88 rattus norv
40	521	32.2	353	11 Q8CJ24	Q8CJ24 mus musculu
41	521	32.2	356	11 Q8CJ23	Q8CJ23 mus musculu
42	515	31.8	155	6 Q9N1E0	Q9N1E0 macaca mula
43	514.5	31.8	291	6 Q8HXE3	Q8HXE3 macaca fasc
44	510.5	31.5	291	11 Q9CR58	Q9CR58 mus musculu
45	501	30.9	337	10 Q9PY68	Q9PY68 arabidopsis

## ALIGNMENTS

RESULT 1  
ID Q7TNY4 PRELIMINARY; PRT; 312 AA.  
AC Q7TNY4;  
DT 01-OCT-2003 (TEMBLrel. 25, Created)  
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
DE Uncoupling protein 3.  
DE Dicostonyx greenlandicus (northern collared lemming).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;  
OC Dicostonyx.  
RN NCBI\_TaxID=85953;  
RX [1]  
RP SEQUENCE FROM N.A.  
RA Blaylock M.L., Wang R., Nagy T.R.;  
RT "Expression of Ucp3 mRNA during weight gain and loss, cold exposure  
RT and fasting in the collared lemming";  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY326457; AAB94991.1; -.  
SQ SEQUENCE 312 AA; 34442 MW; 6EBAF7F4EAB62DE5 CRC64;

Query Match Score 84.6%; DB 11; Length 312;  
Best Local Similarity 84.8%; Pred. No. 3.1e-120;  
Matches 268; Conservative 17; Mismatches 23; Indels 8; Gaps 3;  
QY 1 MWGLKPSDVPPTMAVKFLGAGTACPADLVTEPLDTAKYRLQIQENQAVQTARLVQYRG 60  
DB 1 MWGLQPSSEVPTTVVFLGATGACFADLLTFPLDTAKYRLQIQENPQAQS---QYRG 57  
QY 61 VLGTTITLWRTSPSPNGVAVGLOROMSPASIRIGLVDSVQVYTPPGADNSSLTRT 120  
DB 58 VLGTTITLWRTSPSPNGVAVGLOROMSPASIRIGLVDSVQVYTPPGEDHSSLAIRI 117  
QY 121 LACCTGAAVTCAGPTDVVKVRFQASIHLPSPSRDRTSGTWDAYRTIAREGVLWK 180  
DB 118 LACCTGAAVTCAGPTDVVKVRFQAMIRIG-TGSRKTRGTADAYRTIAREGVLWK 176  
QY 181 GTLPNIRNAIVNCAEVVTYDIILKEKLIDYHLITDNPCHFEVSAFGAGFCATVVASPVV 240



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Db      177 GTWPITENAINVNCMEWYTDIIEKELDSLFTNPFCHFYSAAGAFCAIVVSPDV 236
Qy      241 VKTRVNSPPGOYFSLDCMIKKNVAOEGPTAFYKGFSTPSFLRSGMNVNMFVYEQLKRA 300
Db      237 VKTRVNSPPGOYFSLDCMIKKNVAOEGPTAFYKGFSTPSFLRSGMNVNMFVYEQLKRA 296
Qy      301 ----LMKVOMLRSESPF 312
Db      297 LESKMKQVLRSESPF 312

RESULT 2
Qy      09ER16 PRELIMINARY; PRT; 299 AA.
AC      09ER16;
DT      01-MAR-2001 (TREMBLrel. 16, Last Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Uncoupling protein 3 (Fragment).
OS      Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Phodopus.
OX      NCBI_TaxID=10044;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Tissue-Brown adipose tissue;
RA      von Praun C., Burkert M., Gessner M., Klingenspor M.,
RT      "Tissue-specific expression and cold-induced mRNA levels of uncoupling
RT      proteins in the Djungarian hamster.";
RL      Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL: AF272425; AAC33985.1; -.
DR      GO: GO:0016021; C: integral to membrane; IEA.
DR      GO: GO:0005743; C: mitochondrial inner membrane; IEA.
DR      GO: GO:0005739; C: mitochondrial inner membrane; IEA.
DR      GO: GO:0005488; F: binding; IEA.
DR      GO: GO:0006839; P: mitochondrial transport; IEA.
DR      GO: GO:0006810; P: transport; IEA.
DR      InterPro: IPR001993; Mitoch. carrier.
DR      InterPro: IPR002067; Mtc. carrier.
DR      InterPro: IPR002030; Mtc. uncoupling.
DR      Pfam: PF00153; mltc. carr. 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PROSITE: PS00215; MITOCH. CARRIER, 3.
KM      Membrane; Transmembrane; Transport.
FT      NON TER 299
SQ      SEQUENCE 299 AA; 32784 MW; ABSC947B4DDC49A0 CRC64;

Query Match 83.3%; Score 1350; DB 11; Length 299;
Beet Local Similarity 86.0%; Pred. No. 2.2e-118;
Matches 259; Conservative 16; Mismatches 22; Indels 4; Gaps 2;

Qy      1 MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLQIOGENQAVQTARLVQYRG 60
Db      1 MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLQIOGENPQTOR---VQYRG 57
Qy      61 VLGITLTWRTGSPSPYNGLVAGLQRQNSPASIRIGLYDSYKQVTPPGADNSSLTTRI 120
Db      58 VLGITLTWRTGSPSPYNGLVAGLQRQNSPASIRIGLYDSYKQVTPPGADNSSLTTRI 117
Qy      121 LAGCTTGAAVAVCAOPTDVVKVRFQASIHLPGRSRKSGTMDAVRTIAREEGVGLMK 180
Db      121 LAGCTTGAAVAVCAOPTDVVKVRFQASIHLPGRSRKSGTMDAVRTIAREEGVGLMK 176
Qy      181 GTLPNIRNAIVNCAEVVYTDILKEKLLDYHLTDNFPCHFYSAAGAFCAIVVSPDV 240
Db      177 GTWPITENAINVNCMEWYTDIIEKELDSLFTNPFCHFYSAAGAFCAIVVSPDV 236
Qy      241 VKTRVNSPPGOYFSLDCMIKKNVAOEGPTAFYKGFSTPSFLRSGMNVNMFVYEQLKRA 300

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Db      237 VKTRVNSPPGOYFSLDCMIKKNVAOEGPTAFYKGFSTPSFLRSGMNVNMFVYEQLKRA 296
Qy      301 L 301
Db      297 L 297

RESULT 3
Qy      07YRF3 PRELIMINARY; PRT; 310 AA.
AC      07YRF3;
DT      01-OCT-2003 (TREMBLrel. 25, Created)
DT      01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Uncoupling protein 2.
OS      Antechinus flavipes (Yellow-footed marsupial mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
OX      NCBI_TaxID=38775;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Tissue=Spleen;
RA      Jaarbroek M., Withers K., Klingenspor M.;
RT      "Identification of UCP2 in the marsupial Antechinus flavipes.";
RL      Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
SQ      EMBL: AY233003; AAP44414.1; -.
SQ      SEQUENCE 310 AA; 33304 MW; 11917916F30E54F CRC64;

Query Match 72.7%; Score 1178; DB 6; Length 310;
Beet Local Similarity 72.6%; Pred. No. 3.4e-102;
Matches 228; Conservative 34; Mismatches 46; Indels 6; Gaps 3;

Qy      1 MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLQIOGENQAV---QTARLVQY 58
Db      1 MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLQIOGENQAVSTTAQY 60
Qy      59 RGVLTGTLTWRTGSPSPYNGLVAGLQRQNSPASIRIGLYDSYKQVTPPGADNSSLTTRI 118
Db      61 RGVLTGTLTWRTGSPSPYNGLVAGLQRQNSPASIRIGLYDSYKQVTPPGADNSSLTTRI 119
Qy      119 RIIAGCTTGAAVAVCAOPTDVVKVRFQASIHLPGRSRKSGTMDAVRTIAREEGVGL 178
Db      120 RIIAGCTTGAAVAVCAOPTDVVKVRFQASIHLPGRSRKSGTMDAVRTIAREEGVGL 176
Qy      179 WKGLTNIRNAIVNCAEVVYTDILKEKLLDYHLTDNFPCHFYSAAGAFCAIVVSPDV 238
Db      177 WKGLTNIRNAIVNCAEVVYTDILKEKLLDYHLTDNFPCHFYSAAGAFCAIVVSPDV 236
Qy      239 DVKTRVNSPPGOYFSLDCMIKKNVAOEGPTAFYKGFSTPSFLRSGMNVNMFVYEQLK 298
Db      237 DVKTRVNSPPGOYFSLDCMIKKNVAOEGPTAFYKGFSTPSFLRSGMNVNMFVYEQLK 296
Qy      299 RALMKVOMLRSESPF 312
Db      297 RALMKVOMLRSESPF 310

RESULT 4
Qy      07ZXN1 PRELIMINARY; PRT; 307 AA.
AC      07ZXN1;
DT      01-JUN-2003 (TREMBLrel. 24, Created)
DT      01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Tissue=embryo;

```

RA Klein S., Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC044682; AAH44682.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0006834; F:catalytic activity; IEA.  
 DR GO; GO:0006833; F:fatty acid biosynthesis; IEA.  
 DR GO; GO:0006839; P:mitochondrial transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000794; Ketoacyl\_synth.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_cari; 3.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR Hypothetical protein.  
 KW SEQUENCE 307 AA; 33446 MW; 9035B1F25A9D1F86 CRC64;

Query Match 72.4%; Score 1173.5; DB 13; Length 307;  
 Best Local Similarity 72.1%; Pred. No. 8.4e-102; Indels 5; Gaps 3;  
 Matches 225; Conservative 35; Mismatches 47;

QY 1 MVLGKSDVPEPTMAVKFLGAGTACFADLVTPPLDPAKVLQIQENQAVQTALVQYRG 60  
 DB 1 MVLGKSDVPEPTMAVKFLGAGTACFADLVTPPLDPAKVLQIQENQAVQTALVQYRG 59  
 QY 61 VLGTITLMTVTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVTPPKADNSSLTTRI 120  
 DB 61 VLGTITLMTVTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVTPPKADNSSLTTRI 118  
 QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGPRSDRKYSGTMDARTTAREEGVGLW 180  
 DB 119 AACCTTGAMAVTCAOPTDVVKVRFQAGAN---SSANRRYKGTMDARTTAREEGVGLW 175  
 QY 181 GLTPNIRNAIVNCAEVYTYDILKEKLDYHLTDNPFCHPVSAFGAGCATVVASPV 240  
 DB 176 GTVPNIRNAIVNCTELVYDILKIDSLIKANIMTDNPFCHFTSAFGAGCATVVASPV 235  
 QY 241 VKTRYNNSPPGQYFSPPLDMIKVNAOEGPTAFYKGFPSFLRIGSNVNVFVYEQDKR 300  
 DB 236 VKTRYNNSAGQYTSALNCALTMFRKEGPRAFYKGFPSFLRIGSNVNVFVYEQDKR 295  
 QY 301 LMKVOMLRSPF 312  
 DB 296 MMSAQSRKAPF 307

RESULT 5  
 Q90X50 PRELIMINARY; PRT; 307 AA.  
 AC Q90X50;  
 DT 01-DEC-2001 (TEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)  
 DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 OS Uncoupling protein UCP.  
 OS Melagris gallinavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.  
 OC NCBI\_TaxID=9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA Brock-Clover C.M., Poch S.M., Richards M.P.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF36811; AAL28138.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrial; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0003743; F:translation initiation factor activity; IEA.  
 DR GO; GO:0006833; P:fatty acid biosynthesis; IEA.  
 DR GO; GO:0006839; P:mitochondrial transport; IEA.  
 DR GO; GO:0006413; P:translational initiation; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000794; Ketoacyl\_synth.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001950; TIF\_SUI1.  
 DR Pfam; PF00153; mito\_cari; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR PROSITE; PS01118; SUI1; 1.  
 DR SEQUENCE 307 AA; 33148 MW; 25656D6E682ECCC CRC64;

Query Match 72.0%; Score 1166.5; DB 13; Length 307;  
 Best Local Similarity 72.1%; Pred. No. 4e-101; Indels 7; Gaps 3;  
 Matches 225; Conservative 38; Mismatches 42;

QY 1 MVLGKSDVPEPTMAVKFLGAGTACFADLVTPPLDPAKVLQIQENQAVQTALVQYRG 60  
 DB 1 MVLGKSDVPEPTMAVKFLGAGTACFADLVTPPLDPAKVLQIQENQAVQTALVQYRG 60  
 QY 61 VLGTITLMTVTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVTPPKADNSSLTTRI 120  
 DB 61 VLGTITLMTVTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVTPPKADNSSLTTRI 120  
 QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGPRSDRKYSGTMDARTTAREEGVGLW 179  
 DB 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGPRSDRKYSGTMDARTTAREEGVGLW 177  
 QY 180 KGLTPNIRNAIVNCAEVYTYDILKEKLDYHLTDNPFCHPVSAFGAGCATVVASPV 239  
 DB 178 KGLTPNIRNAIVNCTELVYDILKIDSLIKANIMTDNPFCHFTSAFGAGCATVVASPV 237  
 QY 240 VKTRYNNSPPGQYFSPPLDMIKVNAOEGPTAFYKGFPSFLRIGSNVNVFVYEQDKR 299  
 DB 238 VKTRYNNSAGQYTSALNCALTMFRKEGPRAFYKGFPSFLRIGSNVNVFVYEQDKR 297  
 QY 300 ALMKVOMLRSPF 311  
 DB 298 VVM---LARSAP 306

RESULT 6  
 Q9R246 PRELIMINARY; PRT; 309 AA.  
 AC Q9R246;  
 DT 01-MAY-2000 (TEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
 DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 OS Uncoupling protein 2.  
 OS UCP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CAST/EI;  
 RX MEDLINE=9269912; PubMed=10337618;  
 RA York B., Truett A.A., Monteiro M.P., Barry S.J., Warden C.H.,  
 RA Niggert J.K., Maddatu T.P., West D.B.;  
 RT "gene-environment interaction: a significant diet-dependent obesity  
 RT locus demonstrated in a congenic segment on mouse chromosome 7.";  
 RL Mamm. Genome 10:457-462 (1999).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AF111999; AAD17199.1; -  
 DR MGI; MGI:109354; UCP2.  
 DR GO; GO:0016021; C:integral to membrane; IEA.







```

Db      1  MWGLKRPDVPPLTVKVLVSAGTACIADIATVTEPLDPAKRLIOIGEKAVTGAAGKGRYKG 60
OY      61  VGLTILMTWRTGSPGSPVNGVLAGIQRMSFASIRIGLVDSKYQVYTPPGADNSLTTIRI 120
Db      61  VGLTILMTWRTGSPGSPVNGVLAGIQRMSFASIRIGLVDSKYQVYTPPGADNSLTTIRI 119
OY      121  IAGCTTGAMAVTCAOPTDVVAVKRFQASIHAGPSRSDRKYSCTMDAYRTIAREEGVGLWK 180
Db      120  IAGCTTGAMAVTCAOPTDVVAVKRFQASIHAGPSRSDRKYSCTMDAYRTIAREEGVGLWK 177
OY      181  GTLPNIMRNAIYNCAEVVYDILKEKLLDYLHLLTDFCHFTSAFAGFCATYVASPVUV 240
Db      178  GTLPNITRNAIYNCAEVVYDILKEKLLDYLHLLTDFCHFTSAFAGFCATYVASPVUV 237
OY      241  VTRRYNNSPPGOYFSPGLDCKIMKVAQEGPTAFYKGPSPFLRIGSNVVMFVYEQLKRA 300
Db      238  VTRRYNNSPPGOYFSPGLDCKIMKVAQEGPTAFYKGPSPFLRIGSNVVMFVYEQLKRA 297
OY      301  LM 302
Db      298  MM 299

```

## RESULT 13

```

OYRPF2  PRELIMINARY; PRT; 274 AA.
ID      OYRPF2
AC      01-OCT-2003 (TREMBLrel. 25, Created)
DT      01-OCT-2003 (TREMBLrel. 25, last sequence update)
DR      01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE      Uncoupling protein 2 (Fragment).
GN      UCP2.
OS      Smithopsis macroura (Stripe-faced dumart).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Metatheria; Dasyuromorpha; Dasyuridae; Smithopsis.
[1]
RP      SOURCE FROM N.A.
RC      TISSUE=Splice;
RA      Jastrow M., Withers K., Klingenspor M.;
RT      Identification of UCP2 in Smithopsis macroura.
RL      Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY232964; AAP45779.1; -.
FT      NON_TER 1
SQ      SEQUENCE 274 AA; 29754 MW; 810DABA382B4A569 CRC64;

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Query Match 63.3%; Score 1026; DB 6; Length 274;  
 Best local similarity 72.2%; Pred. No. 5.4e-88;  
 Matches 200; Conservative 32; Mismatches 41; Indels 4; Gaps 3;

```

OY      37  AKRRLIOIGENQ-AVOTARLVQYRGVLTITLMTWRTGSPGSPVNGVLAGIQRMSFASIR 95
Db      1  AKRRLIOIGENQ-AVOTARLVQYRGVLTITLMTWRTGSPGSPVNGVLAGIQRMSFASIR 60
OY      96  IGLYDSVKQVYTPPKGADNSLTTIRIAGCTTGAMAVTCAOPTDVVAVKRFQASIHAGPSRS 155
Db      61  IGLYDSVKQVYTPPKGADNSLTTIRIAGCTTGAMAVTCAOPTDVVAVKRFQASIHAGPSRS 117
OY      156  DRKYSCTMDAYRTIAREEGVGLMKGTLPNIMRNAIYNCAEVVYDILKEKLLDYLHLLT 215
Db      118  SRRYQGTMDAYRTIAREEGVGLMKGTLPNIMRNAIYNCAEVVYDILKEKLLDYLHLLT 177
OY      216  NFPCHEVSAFAGFCATVVASPVVDVVKTRYNNSPPGOYFSPGLDCKIMKVAQEGPTAFYKG 275
Db      178  DLPCHEVSAFAGFCATVVASPVVDVVKTRYNNSATGQYAGAGHCAITMLKESGPQAFYKG 237
OY      276  FTSPFLRIGSNVVMFVYEQLKRALMKVQMLRESPP 312
Db      238  FMPSFLRIGSNVVMFVYEQLKRALMAARTSREVP 274

```

## RESULT 14

```

OYXSEI  PRELIMINARY; PRT; 273 AA.
ID      OYXSEI
AC      01-NOV-1999 (TREMBLrel. 12, Created)
DT      01-NOV-1999 (TREMBLrel. 12, last sequence update)
DR      01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE      Uncoupling protein 2 (Fragment).
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
[1]
RP      SOURCE FROM N.A.
RA      Stone R.T., Rexroad C.E., Smith T.P.L.;
RT      "Bovine UCP2 and UCP3 map to BTA15."
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF127029; AAD29672.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR      GO; GO:0005739; C:mitochondrion; IEA.
DR      GO; GO:0005488; F:binding; IEA.
DR      GO; GO:0006839; P:mitochondrial transport; IEA.
DR      GO; GO:006810; P:transport; IEA.
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002030; Mit_ uncoupling.
DR      Pfam; PF00153; mito_cartr_3.
DR      PRINTS; PR00784; MTUNCOUPLING.
DR      PROSITE; PS000215; MITOCH_CARRIER; 2.
FT      NON_TER 1
SQ      SEQUENCE 273 AA; 29638 MW; 40DAFCB47AAB48 CRC64;

```

Query Match 62.0%; Score 1004.5; DB 6; Length 273;  
 Best local similarity 71.5%; Pred. No. 5.6e-86;  
 Matches 198; Conservative 29; Mismatches 45; Indels 5; Gaps 3;

```

OY      37  AKRRLIOIGENQ-AVOTARLVQYRGVLTITLMTWRTGSPGSPVNGVLAGIQRMSFASIR 95
Db      1  AKRRLIOIGENQ-AVOTARLVQYRGVLTITLMTWRTGSPGSPVNGVLAGIQRMSFASIR 60
OY      96  IGLYDSVKQVYTPPKGADNSLTTIRIAGCTTGAMAVTCAOPTDVVAVKRFQASIHAGPSRS 155
Db      61  IGLYDSVKQVYTPPKGADNSLTTIRIAGCTTGAMAVTCAOPTDVVAVKRFQASIHAGPSRS 116
OY      156  DRKYSCTMDAYRTIAREEGVGLMKGTLPNIMRNAIYNCAEVVYDILKEKLLDYLHLLT 215
Db      117  GRRYQGTMDAYRTIAREEGVGLMKGTLPNIMRNAIYNCAEVVYDILKEKLLDYLHLLT 176
OY      216  NFPCHEVSAFAGFCATVVASPVVDVVKTRYNNSPPGOYFSPGLDCKIMKVAQEGPTAFYKG 275
Db      177  DLPCHEVSAFAGFCATVVASPVVDVVKTRYNNSALQYSSAGHCAITMLKESGPQAFYKG 236
OY      276  FTSPFLRIGSNVVMFVYEQLKRALMKVQMLRESPP 312
Db      237  FMPSFLRIGSNVVMFVYEQLKRALMAARTSREVP 273

```

## RESULT 15

```

OYXSEI  PRELIMINARY; PRT; 193 AA.
ID      OYXSEI
AC      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, last sequence update)
DR      01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE      Uncoupling protein 3 (Fragment).
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecoidea; Macaca.
[1]
RP      SOURCE FROM N.A.

```



RA Thompson G.M., Kelly L.J., Candeloire M.R.;  
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.  
 CC -! SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AF202131; AAF34907.1; -.  
 DR GO: GO:0016021; C: integral to membrane; IEA.  
 DR GO: GO:0005743; C: mitochondrial inner membrane; IEA.  
 DR GO: GO:0005739; C: mitochondrial inner membrane; IEA.  
 DR GO: GO:0005488; F: binding; IEA.  
 DR GO: GO:0006839; P: mitochondrial transport; IEA.  
 DR GO: GO:0006810; P: transport; IEA.  
 DR InterPro: IPR001933; Mitoch\_carrier.  
 DR InterPro: IPR002030; Mlt\_uncoupling.  
 DR Pfam: PF00153; mito\_carr; 2.  
 DR PRINTS: PR00784; MTNCOUPLING.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 2.  
 KW Membrane; Transmembrane; Transport.  
 FT NON\_TER 1  
 FT TER 193  
 SQ SEQUENCE 193 AA; 20730 MW; 5D840DB668091DD CRC64;

Query Match 57.3%; Score 929; DB 6; Length 193;  
 Best Local Similarity 95.3%; Pred. No. 4.4e-79;  
 Matches 183; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

```
QY 15 VKFLGAGTAACPADLVTFPLDPAKVRLOIQENQAVOTARLYQYRGVLTITLTMVTEGP 74
   |||||
Db 2 VKFLGAGTAACPADLVTFPLDPAKVRLOIQENQAVOTARLYQYRGVLTITLTMVTEGP 61
   |||||

QY 75 CSPYNGLVAGLQROMSFPASIRIGLYDSVKQVTPKADNSSLTTRILAGCTTGAMAVTCA 134
   |||||
Db 62 CSPYNGLVAGLQROMSFPASIRIGLYDSVKQVTPKADNSSLTTRILAGCTTGAMAVTCA 121
   |||||

QY 135 OPTDVVXKRFQASIHGSPSRDPKXSGTMDAARTIAREEGVRLKMGTLPNIMRNAIVNC 194
   |||||
Db 122 OPTDVVXKRFQASIHGSSGSDPKXSGTMDAARTIAREEGVRLKMGTLPNIMRNAIVNC 181
   |||||

QY 195 AEVVTYDILKEK 206
   |||||
Db 182 AEVVTYDILKEK 193
   |||||
```

Search completed: May 17, 2004, 11:52:53  
 Job time : 47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OK protein - protein search, using sw model

Run on: May 17, 2004, 11:49:15 ; Search time 17 Seconds  
(without alignments)  
955.640 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620  
Sequence: 1 MVGLKPSDVPPPMAYKFLGA.....TYEQKRALMKYMLRESPP 312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	100.0	312	1	UCP3_HUMAN
2	1492.5	92.1	311	1	UCP3_CANFA
3	1457	89.9	308	1	UCP3_PIG
4	1419.5	87.6	311	1	UCP3_BOVIN
5	1386	85.6	308	1	UCP3_RAT
6	1373	84.8	308	1	UCP3_MOUSE
7	1165.5	71.9	309	1	UCP2_MOUSE
8	1160.5	71.6	309	1	UCP2_PIG
9	1156.5	71.4	309	1	UCP2_RAT
10	1149.5	71.0	309	1	UCP2_HUMAN
11	1145.5	70.7	309	1	UCP2_CANFA
12	1121	69.2	310	1	UCP2_CYPCA
13	1117	69.0	310	1	UCP2_BRARA
14	919	56.7	306	1	UCP1_RABIT
15	902.5	55.7	307	1	UCP1_HUMAN
16	898.5	55.5	306	1	UCP1_RAT
17	885.5	54.7	306	1	UCP1_MOUSE
18	869.5	53.7	306	1	UCP1_MSAU
19	846	52.2	288	1	UCP1_BOVIN
20	521	32.2	325	1	UCP5_MOUSE
21	512	31.6	325	1	UCP5_HUMAN
22	475.5	29.4	323	1	UCP4_HUMAN
23	444	27.4	313	1	M2OM_MOUSE
24	432	26.7	313	1	M2OM_BOVIN
25	426	26.3	313	1	M2OM_RAT
26	416.5	25.7	287	1	DIC_MOUSE
27	415.5	25.6	287	1	DIC_HUMAN
28	327.5	20.2	324	1	OAC1_YEAST
29	293	18.1	322	1	SFC1_YEAST
30	273	16.9	301	1	MCAT_MOUSE
31	272.5	16.8	311	1	TXTP_RAT
32	267	16.5	298	1	ADT3_BOVIN
33					

34	265	16.4	298	1	ADT3_HUMAN	P12236 homo sapien
35	258	15.9	297	1	ADT1_BOVIN	P02722 bos taurus
36	258	15.9	301	1	MCAT_RAT	P97521 rattus norv
37	257	15.9	298	1	ADT1_MOUSE	P48962 mus musculu
38	257	15.9	301	1	MCAT_HUMAN	O43772 homo sapien
39	256.5	15.8	373	1	Y1A6_YEAST	P40556 saccharomyc
40	256	15.8	298	1	ADT2_HUMAN	P05141 homo sapien
41	256	15.8	300	1	MCAT_ARATH	O93xm7 arabidopsis
42	253	15.6	298	1	ADT2_MOUSE	P51881 mus musculu
43	252.5	15.6	311	1	TXTP_BOVIN	P79110 bos taurus
44	252.5	15.6	311	1	TXTP_HUMAN	P53007 homo sapien
45	252.5	15.6	339	1	ADT_CHLKE	P31692 chlorella k

## ALIGNMENTS

RESULT 1	UCP3_HUMAN	STANDARD;	PRT;	312 AA.
AC	P55916; O60475; Q96HU3;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Mitochondrial uncoupling protein 3 (UCP 3).			
GN	UCP3 OR SLC5A9.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	[1]			
RN	TISSUE: SKELETAL MUSCLE;			
RP	TISSUE: SKELETAL MUSCLE;			
RC	MEDLINE=97424095; PubMed=9180264;			
RX	Boss O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J.,			
RA	Rossier C., Muzzin P., Giacobino J.-P.,			
RT	"Uncoupling protein-3: a new member of the mitochondrial carrier			
RT	family with tissue-specific expression."			
RL	FEBS Lett. 408:39-42(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS UCP3L AND UCP3S).			
RX	MEDLINE=97450925; PubMed=9305859;			
RA	Gong D.-W., He Y., Karas W., Reisman M.,			
RT	"Uncoupling protein-3 is a mediator of thermogenesis regulated by			
RT	thyroid hormone, beta3-adrenergic agonists, and leptin."			
RL	J. Biol. Chem. 272:24129-24132(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98158426; PubMed=9498661;			
RA	Uthamer S.A., Dalgaard L.T., Soerensen T.I.A., Tybjaerg-Hansen A.,			
RT	Echwald S.M., Andersen T., Clausen J.O., Pedersen O.,			
RT	"Organisation of the coding exons and mutational screening of the			
RT	uncoupling protein 3 gene in subjects with juvenile-onset obesity."			
RL	Diabetologia 41:241-244(1998).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=10958796;			
RA	Bieberhaer H., Oberkofler H., Krempner F., Strosberg A.D., Patsch W.,			
RT	"The uncoupling protein-3 gene is transcribed from tissue-specific			
RT	promoters in humans but not in rodents."			
RL	J. Biol. Chem. 275:36394-36399(2000).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RC	TISSUE: SKELETAL MUSCLE;			
RX	MEDLINE=22388257; PubMed=12477932;			



```

Db      241 VKTRYNSPPGQYFSPFLDCMIMVNAOEGPTAFYKGTPTSPFLRLGSMNVMMFTYEQLKRA 300
QY      301 LMKVQMLRESPP 312
        |||||
Db      301 LMKVQMLRESPP 312

RESULT 2
UCP3 CANPA STANDARD; PRT; 311 AA.
ID      UCP3 CANPA STANDARD; PRT; 311 AA.
AC      09N219; 09T59;
DT      16-OCT-2001 (rel. 40, Last sequence update)
DT      16-OCT-2001 (rel. 40, Last sequence update)
DT      10-OCT-2003 (rel. 42, Last annotation update)
DE      Mitochondrial uncoupling protein 3 (UCP 3).
GN      UCP3.
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Carnivora; Fissipedes; Canidae; Canis.
RN      NCB1_TaxID=9615;
RP      SEQUENCE FROM N.A.
RA      Ishiooka K.;
RT      "Cloning of canine UCP families.";
RL      Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN      SEQUENCE OF 14-146 FROM N.A.
RP      Thompson G.M., Kelly L.J., Candelore M.R.;
RA      Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC      PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
CC      UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
CC      DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
CC      OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
CC      ENERGY BALANCE (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane (By similarity).
CC      -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -1- SIMILARITY: Contains 3 Solcar repeats.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB022020; BAA90458.1; -.
DR      EMBL; AF201378; AAF08310.1; -.
DR      InterPro; IPR002030; MLC_uncoupling.
DR      InterPro; IPR001993; Mitoch_carrier.
DR      Pfam; PF00153; mito_carri; 3.
DR      PRINTS; PR00784; MTUNCoupling.
DR      PROSITE; PS00920; SOLCAR; 3.
KW      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT      TRANSMEM 11
FT      TRANSMEM 77
FT      TRANSMEM 99
FT      TRANSMEM 120
FT      TRANSMEM 183
FT      TRANSMEM 217
FT      TRANSMEM 271
FT      REPEAT 11
FT      REPEAT 105
FT      REPEAT 114
FT      REPEAT 299
FT      DOMAIN 278
FT      DOMAIN 300
FT      CONFLICT 14
SQ      SEQUENCE 311 AA; 34137 MW; A719PB8D66537502 CRC64;
Query Match 92.1%; Score 1492.5; DB 1; Length 311;
Best Local Similarity 91.7%; Pred. No. 2,9e-129;
Matches 286; Conservative 14; Mismatches 11; Indels 1; Gaps 1;

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QY      1 MWGLKSPDVPPTMAVYKPIGAGTACPADLVTEPLDTAKVRLQIOGENQAVQTAFLVQYRG 60
Db      1 MWGLKSPDVPPTTAAVYKPIGAGTACPADLVTEPLDTAKVRLQIOGENQAVQTAFLVQYRG 60
QY      61 VLGTLITWRTGSPSPYNGVLVAGLQROMSPASIRIGLYDSKVQYTPFGADNSLTTR 120
Db      61 VLGTLITWRTGSPSPYNGVLVAGLQROMSPASIRIGLYDSKVQYTPFGADNSLTTR 120
QY      121 LAGCTGAAVATCAOPTDVYKTRFQASIHLCGSRSPRKSCTMDARTTAREGVGLWK 180
Db      121 LAGCTGAAVATCAOPTDVYKTRFQASIHLCGSRSPRKSCTMDARTTAREGVGLWK 180
QY      181 GLTPNTRAAVYNCADVLYYDILKEKLDLHYHLLTNPCHPVSAFGAGCATVVASPV 240
Db      180 GLTPNTRAAVYNCADVLYYDILKEKLDLHYHLLTNPCHLVSAFGAGCATVVASPV 239
QY      241 VKTRYNSPPGQYFSPFLDCMIMVNAOEGPTAFYKGTPTSPFLRLGSMNVMMFTYEQLKRA 300
Db      240 VKTRYNSPPGQYFSPFLDCMIMVNAOEGPTAFYKGTPTSPFLRLGSMNVMMFTYEQLKRA 299
QY      301 LMKVQMLRESPP 312
Db      300 LMKVQMLRESPP 311

RESULT 3
UCP3 PIG STANDARD; PRT; 308 AA.
ID      UCP3 PIG STANDARD; PRT; 308 AA.
AC      097649; 09X56;
DT      30-MAY-2000 (rel. 39, Last sequence update)
DT      30-MAY-2000 (rel. 39, Last sequence update)
DT      10-OCT-2003 (rel. 42, Last annotation update)
DE      Mitochondrial uncoupling protein 3 (UCP 3).
GN      UCP3.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN      NCB1_TaxID=9823;
RP      SEQUENCE FROM N.A.
RA      TISSUE=White adipose tissue;
RC      Werner P., Nowaczky K., Neuenschwander S., Strazinger G.;
RT      "Characterization of the porcine uncoupling proteins 2 and 3 (UCP2 &
RT      3) and their localization to chromosome 9p by somatic cell hybrids.";
RL      Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN      SEQUENCE FROM N.A.
RP      STRAIN=Large white X Pietrain; TISSUE=Skeletal muscle;
RC      Damon M., Vincent A., Herpin P.;
RT      "First evidence of uncoupling protein (UCP) gene expression in piglet
RT      skeletal muscle.";
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
CC      PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
CC      UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
CC      DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
CC      OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
CC      ENERGY BALANCE (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane (By similarity).
CC      -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -1- SIMILARITY: Contains 3 Solcar repeats.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF095744; AAD08811.1; -.

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DR EMBL; AF128837; AAD33396.1; -;  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3\_  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 74 96 2 (POTENTIAL).  
 FT TRANSMEM 117 133 3 (POTENTIAL).  
 FT TRANSMEM 180 196 4 (POTENTIAL).  
 FT TRANSMEM 214 233 5 (POTENTIAL).  
 FT TRANSMEM 268 290 6 (POTENTIAL).  
 FT REPEAT 11 102 SOLCAR 1.  
 FT REPEAT 111 202 SOLCAR 2.  
 FT REPEAT 211 286 SOLCAR 3.  
 FT DOMAIN 215 297 SOLCAR 3.  
 FT CONFLICT 7 8 PE -> SD (IN REF. 2).  
 FT CONFLICT 13 13 T -> M (IN REF. 2).  
 FT CONFLICT 17 17 L -> R (IN REF. 2).  
 FT CONFLICT 49 49 A -> AVGT (IN REF. 2).  
 FT CONFLICT 150 150 R -> G (IN REF. 2).  
 SQ SEQUENCE 308 AA; 33772 MW; FDFLP2BC28FDE997 CRC64;

Query Match 89.9%; Score 1457; DB 1; Length 308;  
 Best Local Similarity 90.1%; Pred. No. 5,1e-126;  
 Matches 281; Conservative 14; Mismatches 13; Indels 4; Gaps 2;

QY 1 MWGLKPSDVPPTMAVYFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 DB 1 MWGLKPSDVPPTMAVYFLGAGTACFADLVTPPLDTAKVRLQIOGENQ---ARSAQYRG 57  
 QY 61 VGTLLTWRTGSPSPNGVAGLQROMSFASIRIGLYDSYKQYTPPGANSSLTTRI 120  
 DB 58 VGTLLTWRTGSPSPNGVAGLQROMSFASIRIGLYDSYKQYTPPGANSSLTTRI 117  
 QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRTKSGTMDAVRTIAREGVRLMK 180  
 DB 118 LAGCTTGAMAVTCAOPTDVVKVRFQASIHAGP-RSRKXSGTMDAVRTIAREGVRLMK 176  
 QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNFPHVSAFGAGCATVVASPVUV 240  
 DB 177 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNLPCHFPVSAFGAGCATVVASPVUV 236  
 QY 241 VTRRYNNSPPGOYFSPLODMIMVNAOEGPTAFYKGTBSPFLRLGSMNVVMFTYEQLKRA 300  
 DB 237 VTRRYNNSPPGOYFSPLODMIMVNAOEGPTAFYKGTBSPFLRLGSMNVVMFTYEQLKRA 296  
 QY 301 LMKVQMLRESPP 312  
 DB 297 LMKVQMLRESPP 308

RESULT 4  
 UC33\_BOVIN  
 ID UC33\_BOVIN STANDARD; PRT; 311 AA.  
 AC 077792; Q9TVA1;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitochondrial uncoupling protein 3 (UCP 3).  
 OS UCP3.  
 GN Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;

RA Stone R.T., Smith T.P.L.;  
 RT "Bovine uncoupling protein 3."  
 RL Submitted (Sep-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-274 FROM N.A., AND VARIANT THR-53.  
 RA Stone R.T., Rexroad C.E., Smith T.P.L.;  
 RT "Bovine UCP2 and UCP3 map to BTA15."  
 RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE  
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS  
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS  
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION  
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND  
 CC ENERGY BALANCE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- SIMILARITY: Contains 3 solcar repeats.  
 CC -----  
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 CC -----  
 DR EMBL; AF092048; AAC61762.1; -;  
 DR EMBL; AF170303; AAD33339.1; -;  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Polymorphism.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 77 99 2 (POTENTIAL).  
 FT TRANSMEM 120 136 3 (POTENTIAL).  
 FT TRANSMEM 183 199 4 (POTENTIAL).  
 FT TRANSMEM 217 236 5 (POTENTIAL).  
 FT TRANSMEM 271 293 6 (POTENTIAL).  
 FT REPEAT 11 105 SOLCAR 1.  
 FT REPEAT 114 205 SOLCAR 2.  
 FT REPEAT 214 299 SOLCAR 3.  
 FT DOMAIN 278 300 PURINE NUCLEOTIDE BINDING (BY  
 FT SIMILARITY).  
 FT VARIANT 53 53 A -> T.  
 SQ SEQUENCE 311 AA; 34205 MW; BLAID26E25650D04 CRC64;

Query Match 87.6%; Score 1419.5; DB 1; Length 311;  
 Best Local Similarity 87.2%; Pred. No. 1.4e-122;  
 Matches 272; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

QY 1 MWGLKPSDVPPTMAVYFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 DB 1 MWGLKPSDVPPTMAVYFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60  
 QY 61 VGTLLTWRTGSPSPNGVAGLQROMSFASIRIGLYDSYKQYTPPGANSSLTTRI 120  
 DB 61 VGTLLTWRTGSPSPNGVAGLQROMSFASIRIGLYDSYKQYTPPGANSSLTTRI 120  
 QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRTKSGTMDAVRTIAREGVRLMK 180  
 DB 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRTKSGTMDAVRTIAREGVRLMK 179  
 QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNFPHVSAFGAGCATVVASPVUV 240  
 DB 180 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNFPHVSAFGAGCATVVASPVUV 239  
 QY 241 VTRRYNNSPPGOYFSPLODMIMVNAOEGPTAFYKGTBSPFLRLGSMNVVMFTYEQLKRA 300

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DB 240 VSTRYNSPPGQYHSPDCMLNMTQEGPTATYKGFTHSFLKLSNNVMMFTYEQMKA 299
OY 301 LMKVQMLRESPP 312
DB 300 LMKVQMLRDSPP 311

RESULT 5
UCP3 RAT STANDARD; PRT; 308 AA.
AC P56499;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RX MEDLINE=98074937; PubMed=9414126;
RA Matsuda J., Hosoda K., Itoh H., Son C., Doi K., Tanaka T.,
RA Fukunaga Y., Inoue G., Mishimura H., Yoshimasa Y., Yamori Y.,
RA Nakao K.;
RT "Cloning of rat uncoupling protein-3 and uncoupling protein-2 cDNAs:
RT their gene expression in rats fed high-fat diet.";
RT FEBS Lett. 418:200-204(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Skeletal muscle;
RX MEDLINE=98165302; PubMed=9506477;
RA Rose O., Samiec S., Desplanches D., Mayet M.-H., Seydoux J., Muzzin P.,
RA Giacobino J.-P.;
RT "Effect of endurance training on mRNA expression of uncoupling
RT proteins 1, 2, and 3 in the rat.";
RT PASEB J. 12:335-339(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RX MEDLINE=98400868; PubMed=9725803;
RA Lin B.-D., Coughlin S., Pilch P.F.;
RT "Bidirectional regulation of uncoupling protein-3 and GLUT-4 mRNA in
RT skeletal muscle by cold.";
RT Am. J. Physiol. 275:E386-E391(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RA Solanes G., Valet P., Lowell B.B.;
RT "Lipopolysaccharide treatment increases thermogenesis and induces
RT uncoupling protein-3 gene expression in skeletal muscle.";
RT Submitted (Oct-1997) to the EMBL/GenBank/DBD databases.
RN [5]
RP FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
RP PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
RP UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
RP DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
RP OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
RP ENERGY BALANCE (BY SIMILARITY).
RN [6]
RP SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
RP inner membrane (By similarity).
RN [7]
RP SIMILARITY: Belongs to the mitochondrial carrier family.
RN [8]
RP SIMILARITY: Contains 3 Solar repeats.
RN [9]
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CC EMBL; AB006614; BAA23355.1; -
DR EMBL; U92069; AAB71523.1; -
DR EMBL; AF035943; AAC05740.1; -
DR EMBL; AF030163; AAD01891.1; -
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR InterPro; IPR001993; Mito_carrier.
DR Pfam; PF00153; mlt_carrier_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS50920; SOLCAR_3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 74 96
FT TRANSMEM 117 133
FT TRANSMEM 180 196
FT TRANSMEM 214 233
FT TRANSMEM 268 290
FT REPEAT 11 102
FT REPEAT 111 202
FT REPEAT 211 296
FT DOMAIN 275 297
FT SQ
SEQUENCE 308 AA; 34014 MW; F86E784530AC555 CRC64;

Query Match 85.6%; Score 1386; DB 1; Length 308;
Best Local Similarity 86.2%; Pred. No. 1.6e-119;
Matches 269; Conservative 17; Mismatches 22; Indels 4; Gaps 2;

OY 1 MTGLKPSDVPPTMYAKYFGAGTACGADLVTEPLDTAKRLIOIGENQAVQTRLVQYRG 60
DB 1 MWGLQSEVPPTTVKVFAGTACGADLVTEPLDTAKRLIOIGENQAVQ---VQYRG 57
OY 61 VLGTLITWRTGSPSPYNGVLVAGLQRCMSFASIRIGLYDSYQVYTPPKGADNSLTTRI 120
DB 58 VLGTLITWRTGSPSPYNGVLVAGLQRCMSFASIRIGLYDSYQVYTPPKGADNSVAIRI 117
OY 121 LAGCTTGAMAVTCAQPTDVYKTRFQASITLGSRSRKRKSGTMDARTTAREGVGLWK 180
DB 118 LAGCTTGAMAVTCAQPTDVYKTRFQASITLGSRSRKRKSGTMDARTTAREGVGLWK 176
OY 181 GLLPNTMRNAIYNCAEVVYDILKEGLDYHLTDNFCGFSAFGAGCATVVASPVDV 240
DB 177 GLLPNTMRNAIYNCAEVVYDILKEGLDYHLTDNFCGFSAFGAGCATVVASPVDV 236
OY 241 VSTRYNSPPGQYHSPDCMLNMTQEGPTATYKGFTHSFLKLSNNVMMFTYEQMKA 300
DB 237 VSTRYNSPPGQYHSPDCMLNMTQEGPTATYKGFTHSFLKLSNNVMMFTYEQMKA 296
OY 301 LMKVQMLRESPP 312
DB 297 LMKVQMLRDSPP 308

RESULT 6
UCP3 MOUSE STANDARD; PRT; 308 AA.
AC P56501; O88293;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sanchez D., Fleury C., Boullaud F., Ricquier D.;
RT Submitted (NOV-1997) to the EMBL/GenBank/DBD databases.

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RN [2] SEQUENCE FROM N.A.  
 RP STRAIN=Swiss Webster; TISSUE=Embryo;  
 RC MEDLINE=98332721; PubMed=9666083;  
 RX Yoshitomi H., Yamazaki K., Tanaka I.,  
 RA "Cloning of mouse uncoupling protein 3 cDNA and 5'-flanking region,  
 RT and its genetic map.";  
 RL Gene 215:77-84(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Skeletal muscle;  
 RA Grubic D., Zhan C.-Y., Sleiker L.J., Lowell B.B.,  
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Skeletal muscle;  
 RA Son C., Hosoda K., Matsuoka J., Nakao K.,  
 RT "Cloning of mouse UCP3 cDNA.";  
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=99167332; PubMed=10066417;  
 RX Gong D.W., He Y., Reitman M.L.,  
 RA "Genomic organization and regulation by dietary fat of the uncoupling  
 RT protein 3 and 2 genes.";  
 RL Biochem. Biophys. Res. Commun. 256:27-32(1999).  
 RN [6]  
 RP SEQUENCE OF 84-180 FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;  
 RX MEDLINE=98262957; PubMed=9600108;  
 RA Shimokawa T., Kato M., Ezaki O., Hashimoto S.,  
 RT "Transcriptional regulation of muscle-specific genes during myoblast  
 RL differentiation.";  
 RN Biochem. Biophys. Res. Commun. 246:287-292(1998).  
 RN [7]  
 RP SEQUENCE OF 162-252 FROM N.A.  
 RA Yan X., Ramsey T.G.,  
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE  
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS  
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION AS A RESULT. ENERGY IS  
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION  
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND  
 CC ENERGY BALANCE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- SIMILARITY: Contains 3 Solcar repeats.  
 CC -----  
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 CC -----  
 CC EMBL: AF032902; AAB87084.1; -  
 CC EMBL: AB010742; BAA25697.1; -  
 CC EMBL: AF030164; AAD01892.1; -  
 CC EMBL: AB008216; BAA33502.1; -  
 CC EMBL: AF053352; AAC28328.1; -  
 CC EMBL: AB011132; BAA31989.1; -  
 CC EMBL: AF019883; AAB71543.1; -  
 CC MGD: MGI:1099787; Ucp3.  
 CC GO: GO:0005739; C:mitochondrion; IMP.  
 CC GO: GO:0015302; F:uncoupling protein activity; IMP.  
 CC GO: GO:0006631; P:fatty acid metabolism; IMP.  
 CC GO: GO:0003033; P:response to superoxide; IMP.  
 CC InterPro: IPR002067; Mlt\_carrier.  
 CC InterPro: IPR002030; Mlt\_uncoupling.  
 CC InterPro: IPR001993; Mltch\_carrier.  
 CC Pfam: PF00153; mltc\_cartr; 3.

DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 74 96 2 (POTENTIAL).  
 FT TRANSMEM 117 133 3 (POTENTIAL).  
 FT TRANSMEM 180 196 4 (POTENTIAL).  
 FT TRANSMEM 214 233 5 (POTENTIAL).  
 FT TRANSMEM 268 290 6 (POTENTIAL).  
 FT REPEAT 11 102 SOLCAR 1.  
 FT REPEAT 111 202 SOLCAR 2.  
 FT REPEAT 211 296 SOLCAR 3.  
 FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY  
 FT SIMILARITY).  
 FT CONFLICT 179 179 W -> L (IN REF. 6).  
 SQ SEQUENCE 308 AA; 33910 MM; 12CAD7674DFD0C3 CRC64;  
 Query Match 84.8%; Score 1373; DB 1; Length 308;  
 Best Local Similarity 85.6%; Pred. No. 2.5e-118;  
 Matches 267; Conservative 18; Mismatches 23; Indels 4; Gaps 2;  
 QY 1 MVGLKPSDVPPTMAVKFAGAGTACFADLVTFPPIDTAKVRLQIGENQAVGTARLVQYRG 60  
 DB 1 MVGLQPSSEVPPTTVKFLGAGTACFADLVTFPPIDTAKVRLQIGENQAGS---VQYRG 57  
 QY 61 VLGITLTVTRTEGSPSPNGVAGLQROMSPASIRIGLYDSVKQVYTPKGDNSLTTTRI 120  
 DB 58 VLGITLTVTRTEGSPSPNGVAGLQROMSPASIRIGLYDSVKQVYTPKGDHSSVAIRI 117  
 QY 121 LAGCTGAMAVTCAQPTDVVVRQASIHGSPSSDKYSGTMAVRYTAAEEGVRIWK 180  
 DB 118 LAGCTTGMAVTCQPTDVVVRQAMIRLG-TGERKRYGTMAVRYTAAEEGVRIWK 176  
 QY 181 GLTNIRKNAIVNCAEVYTDYLKEKLLDYHLTDNPFCHFSVAFGAGFCATVVASPDV 240  
 DB 177 GTWENIRNAIVNCAENVYTDIIEKLLBSLTFDNPCHFSVAFGAGFCATVVASPDV 236  
 QY 241 VKTRYMNSPQGYSPPLDCMKVAQSGPTAFYKGTPTSPFLRLGSNNVVFYTYEQLKRA 300  
 DB 237 VKTRYMNAFLGRYSPPLDCMKVAQSGPTAFYKGFVPSFLRLGAMNMVFYTYEQLKRA 296  
 QY 301 LMKQVLMRESPP 312  
 DB 297 LMKQVLMRESPP 308  
 RESULT 7  
 UCP2\_MOUSE STANDARD, PRT, 309 AA.  
 AC P70406; O88285;  
 ID UCP2\_MOUSE  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Mitochondrial uncoupling protein 2 (UCP 2) (UCHN).  
 GN UCP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Muscle;  
 RA Raimbault S., Bouillaud F., Ricquier D.,  
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=97278985; PubMed=9133562;  
 RA Gimeno R.E., Dembski M., Weng X., Deng N., Shyjan A.W.,  
 RA Gimeno C.J., Iris F., Ellis S.J., Woolf E.A., Taragila L.A.,  
 RT "Cloning and characterization of an uncoupling protein homolog: a  
 RT potential molecular mediator of human thermogenesis."

Diabetes 46:900-906(1997).  
 [3]  
 RA SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA;  
 RC MEDLINE=96374026; PubMed=9710252;  
 RA Yamada M., Hashida T., Shibusawa N., Iwasaki T., Murakami M.,  
 RA Menden T., Satoh T., Mori M.;  
 RA "Genomic organization and promoter function of the mouse uncoupling  
 RT protein 2 (UCP2) gene."  
 RL FEBS Lett. 432:65-69(1998).  
 [4]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Colon, and Mammary gland;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Straube R.L., Fellingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schler G.D.,  
 RA Altschul S.F., Zeebber B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.U., Malek U.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schultz R.W.,  
 RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create  
 CC proton leaks across the inner mitochondrial membrane, thus  
 CC uncoupling oxidative phosphorylation from ATP synthesis. As a  
 CC result, energy is dissipated in the form of heat (By similarity).  
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: HIGHEST IN WHITE ADIPOSE TISSUE BUT ALSO  
 CC DETECTED IN BROWN ADIPOSE TISSUE, HEART, AND KIDNEY. 4-6 TIMES  
 CC HIGHER LEVELS ARE DETECTED IN OB/OB AND DB/DB MICE.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- SIMILARITY: Contains 3 Solcar repeats.  
 CC -----  
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 CC -----  
 CC EMBL: U69135; AAB17666.1; -;  
 DR EMBL: U94593; AAB53092.1; -;  
 DR EMBL: AB012159; BA332532.1; -;  
 DR EMBL: BC012697; AAH12697.1; -;  
 DR EMBL: BC012967; AAH12967.1; -;  
 DR MGD: MGI:109354; UCP2.  
 DR InterPro: IPR002030; Mit uncoupling.  
 DR InterPro: IPR001993; Mitoch. carrier.  
 DR Pfam: PF00153; mito\_carri\_3.  
 DR PRINTS: PRO0784; MTUNCOUPLING.  
 DR PROSITE: PS50920; SOLCAR; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 78 100 2 (POTENTIAL).  
 FT TRANSMEM 120 136 3 (POTENTIAL).  
 FT TRANSMEM 181 197 4 (POTENTIAL).  
 FT TRANSMEM 215 234 5 (POTENTIAL).  
 FT TRANSMEM 269 291 6 (POTENTIAL).

FT REPEAT 11 106 SOLCAR 1.  
 FT REPEAT 114 203 SOLCAR 2.  
 FT REPEAT 212 297 SOLCAR 3.  
 FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY  
 FT CONFLICT 285 285 V -> I (IN REF. 3).  
 FT SEQUENCE 309 AA; 33373 MW; 329794EBA99810E5 CRC64;  
 Query Match 71.9%; Score 1165.5; DB 1; Length 309;  
 Best Local Similarity 72.8%; Pred. No. 2.6e-99;  
 Matches 228; Conservative 31; Mismatches 49; Indels 5; Gaps 3;  
 QY 1 NVGLKPSVDPPTMAVKFAGATACGADLVTEPDTAKRLQIQENQA-VQIARLVQYR 59  
 DB 1 NVGFRATDVPPTATKVFAGATACIADITFPDTAKRLQIQESQGLVTTAASQYR 60  
 QY 60 GVLGTLITMVRREGGCSPPNGVVALQROMSPASIRIGLYSDVKQYVTPKGDNSLTTR 119  
 DB 61 GVLGTLITMVRREGGSRSLNGVVALQROMSPASIRIGLYSDVKQYVTPKGDNSLTTR 119  
 QY 120 ILAGCTGMAVTCAPTDVVVVRFOASITLQPSRSDRKSQGTMDAYRTIAREEGVRLM 179  
 DB 120 ILAGSTTGALAVAVAPDIDVAVKVRQQAQARAG--GGRYVSTVETAKYTIAREEGRLM 176  
 QY 180 KGTLPINEMNAIVNCAEVYVDILKLDVHLITDNFPCHFVSAFAGFCATVVASPD 239  
 DB 177 KGTSPVARNNAIVNCAELVYVDILKOTLLKANLMTDILPCHFTSAFAGFCCTVIASPD 236  
 QY 240 VKTRYNMSPPCQYSPIDCMIKMAVQSGPTAFYFGFTSPFRLGSMVMVTVYQLKR 299  
 DB 237 VKTRYNMSPALQYVSHAGCALITMLRKGPAPFAFYGFSPFLRLGSMVMVTVYQLKR 296  
 QY 300 ALMKVQMLRESPE 312  
 DB 297 ALMAAYQSHREAP 309  
 RESULT 8  
 ID UCP2\_PIG STANDARD; PRT; 309 AA.  
 AC 097562; Q96K29;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitochondrial uncoupling protein 2 (UCP 2).  
 GN UCP2.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Suidae.  
 OX NCBI\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=white adipose tissue;  
 RA Werner P., Nowaczyk K., Neuenschwander S., Strazinger G.;  
 RT "Characterization of the porcine uncoupling proteins 2 and 3 (UCP2 &  
 RT 3) and their localization to chromosome 9p by somatic cell hybrids";  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBD databases.  
 RN [2]  
 RP SEQUENCE OF 114-211 FROM N.A.  
 RA Fang M.-Y., Zhao X.-B., Li N.;  
 RT "Exon 3, Intron 3 and exon 4 sequencing of porcine uncoupling protein  
 RT 2 gene";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBD databases.  
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create  
 CC proton leaks across the inner mitochondrial membrane, thus  
 CC uncoupling oxidative phosphorylation from ATP synthesis. As a  
 CC result, energy is dissipated in the form of heat (By similarity).  
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- SIMILARITY: Contains 3 Solcar repeats.  
 CC -----

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL; AF036757; AAC05201.1; -  
DR EMBL; AF332003; AAG45440.1; -  
DR InterPro; IPR002030; Mit-uncoupling.  
DR InterPro; IPR001993; Mitoch. carrier.  
DR Pfam; PF00153; mito. carr; 3.  
DR PRINTS; PR00784; MTUNCOUPLING.  
DR PROSITE; PS50920; SOLCAR; 3.

KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 11 32 1 (POTENTIAL).  
FT TRANSMEM 78 100 2 (POTENTIAL).  
FT TRANSMEM 120 136 3 (POTENTIAL).  
FT TRANSMEM 181 197 4 (POTENTIAL).  
FT TRANSMEM 215 234 5 (POTENTIAL).  
FT TRANSMEM 269 291 6 (POTENTIAL).  
FT REPEAT 11 106 SOLCAR 1.  
FT REPEAT 114 203 SOLCAR 2.  
FT REPEAT 212 297 SOLCAR 3.  
FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY  
FT SIMILARITY).

FT CONFLICT 115 115 G -> S (IN REF. 2).  
FT CONFLICT 208 208 D -> N (IN REF. 2).  
SQ SEQUENCE 309 AA; 33259 MW; 7A67D59946DA21BD CRC64;

Query Match  
Best Local Similarity 71.6%; Score 1160.5; DB 1; Length 309;  
Matches 227; Conservative 30; Mismatches 51; Indels 5; Gaps 3;

QY 1 MVGLKPSDVPPTMAVVFELAGTAACPADLVTEPLDTAKVRLQIQEENQ-VQTAFLVQR 59  
DB 1 MVGFATKTEVPATVAFELAGTAACPADLVTEPLDTAKVRLQIQEENQVQTAFLVQR 60  
QY 60 GVLGTLVWRTGEPSPNGVAVGQROMSPASITIGLYDSKQVYTKKADNSLTTR 119  
DB 61 GVLGTLVWRTGEPSPNGVAVGQROMSPASITIGLYDSKQVYTKKADNSLTTR 119  
QY 120 ILAGCTTGAAVTCACPTDVVKVRFQASVHLGPRSDRKSGTMDAYRTIAEEGVGLM 179  
DB 120 ILAGCTTGAAVTCACPTDVVKVRFQASVHLGPRSDRKSGTMDAYRTIAEEGVGLM 176  
QY 180 KGLTPNIMENAIYVCAEVVYDILKELLDYHLITDNFCHVSAFGACFCATVVASPYD 239  
DB 177 KGLTPNIMENAIYVCAEVVYDILKELLDYHLITDNFCHVSAFGACFCATVVASPYD 236  
QY 240 VVKTRTMSBPQGYFPLDQMTQVAVQEGPTAFYKGFSTFSLTSGMNVVMTVYRQLR 299  
DB 237 VVKTRTMSBPQGYFPLDQMTQVAVQEGPTAFYKGFSTFSLTSGMNVVMTVYRQLR 296  
QY 300 ALMKVQLRESPPF 312  
DB 297 ALMKVQLRESPPF 309

RESULT 9  
UCP2\_RAT STANDARD; PRT; 309 AA.  
AC P565F0; 070178; 088183;  
DT 15-UTR-1998 (Rel. 36, Created)  
DT 15-UTR-1998 (Rel. 36, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Mitochondrial uncoupling protein 2 (UCP 2).  
GN UCP2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=White adipose tissue;  
RA Strobel A., Stroberg A.D., Issad T.;  
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brown adipose tissue;  
RX MEDLINE=98074937; PubMed=9414126;  
RA Matsuda J., Hosoda K., Itoh H., Son C., Doi K., Tanaka T.,  
RA Fukunaga Y., Inoue G., Nishimura H., Yoshimasa Y., Yamori Y.,  
RA Nakao K.;  
RT "Cloning of rat uncoupling protein-3 and uncoupling protein-2 cDNAs:  
RT their gene expression in rats fed high-fat diet.";  
RL FEBS Lett. 418:200-204(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Spleen;  
RA Yamazaki K., Yoshimoto H., Tanaka T.;  
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mouse; TISSUE=Brain;  
RX MEDLINE=98173791; PubMed=9512646;  
RA Hidaka S., Kakuma T., Yoshimatsu H., Yasunaga S., Kurokawa M.,  
RA Sakata T.;  
RT "Molecular cloning of rat uncoupling protein 2 cDNA and its expression  
RT in genetically obese Zucker fatty (fa/fa) rats.";  
RL Biochim. Biophys. Acta 1389:178-186(1998).  
CC -1- FUNCTION: UCP acts as mitochondrial transporter proteins that create  
CC proton leaks across the inner mitochondrial membrane, thus  
CC uncoupling oxidative phosphorylation from ATP synthesis. As a  
CC result, energy is dissipated in the form of heat (By similarity).  
CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane.  
CC -1- TISSUE SPECIFICITY: Expressed in a variety of organs, with  
CC predominant expression in the heart, lung and spleen.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC -1- SIMILARITY: Contains 3 Solcar repeats.  
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CC EMBL; AF036757; AAC98733.1; -  
CC EMBL; AB006613; BAA23383.1; -  
CC EMBL; AB0010743; BAA25698.1; -  
CC EMBL; AB005143; BAA28832.1; -  
CC InterPro; IPR002030; Mit-uncoupling.  
CC InterPro; IPR001993; Mitoch. carrier.  
CC Pfam; PF00153; mito. carr; 3.  
CC PRINTS; PR00784; MTUNCOUPLING.  
CC PROSITE; PS50920; SOLCAR; 3.  
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
FT TRANSMEM 11 32 1 (POTENTIAL).  
FT TRANSMEM 78 100 2 (POTENTIAL).  
FT TRANSMEM 120 136 3 (POTENTIAL).  
FT TRANSMEM 181 197 4 (POTENTIAL).  
FT TRANSMEM 215 234 5 (POTENTIAL).  
FT TRANSMEM 269 291 6 (POTENTIAL).  
FT REPEAT 11 106 SOLCAR 1.  
FT REPEAT 114 203 SOLCAR 2.  
FT REPEAT 212 297 SOLCAR 3.  
FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY  
FT SIMILARITY).

FT CONFLICT 9 9 V -> L (IN REF. 4).  
FT CONFLICT 268 268 A -> T (IN REF. 3).  
SQ SEQUENCE 309 AA; 33376 MW; 3297935CF97AA0E CRC64;

Query Match 71.4%; Score 1156.5; DB 1; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 1.7e-98;  
 Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;

QY 1 MWGLKSDVPTMAVAVFLAGTACPADLVTEPLDTAKVRLQIQENQAV-QTARLVQYR 59  
 1 MWGPKATDVPATATVAFVFLGAGTACIADITPLDTAKVRLQIQENQAVQYR 60  
 DB 60 GVLGTLTVNRTEGCPSPNGVLVAGIQRQMSFASITIGLYDSKYQYTPKGNSSLTTR 119  
 61 GVLGTLTVNRTEGCPSPNGVLVAGIQRQMSFASITIGLYDSKYQYTPKGNSSLTTR 119  
 DB 120 ILAAGCTGMAVATCAPTDVVKVRFOASITLGPSSDRKSGTMDVYRTAREEGVGLM 179  
 120 LLAAGTTGALAAVAVOPTDVVKVRFOAQARAG---GGRYQSTVEAYKTIAREEGVGLM 176  
 QY 180 KGTLPINENAVINCAVAVYTYDILKEKLDYHLLTDFPCFVSAFAGCATVAVSPVD 239  
 177 KGTSPVAVANAIINCELVYTYDILKEKLDYHLLTDFPCFVSAFAGCATVAVSPVD 236  
 DB 240 VVKTRFMNSPPQYFEPFLDMIMQAQEGPTAFYKGTBSFLGSMVNMVMTTYEQLR 239  
 237 VVKTRFMNSPPQYFEPFLDMIMQAQEGPTAFYKGTBSFLGSMVNMVMTTYEQLR 236  
 QY 300 ALMKVQMLRESPP 312  
 297 ALMAAYESREAPP 309

RESULT 10  
 UC2P2\_HUMAN STANDARD; PRT; 309 AA.  
 ID UC2P2\_HUMAN STANDARD; PRT; 309 AA.  
 AC P55851;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitochondrial uncoupling protein 2 (UCP 2) (UCPF).  
 GN UCP2 OR SLC25A8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA MEDLINE=97324095; PubMed=9180264;  
 RA Boss O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J.,  
 RA Rossier C., Muzzin P., Giacobino J.-P.;  
 RT "uncoupling protein-3: a new member of the mitochondrial carrier  
 RT family with tissue-specific expression.";  
 RL FEBS Lett. 408:39-42(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung, and Skeletal muscle;  
 RA MEDLINE=97207646; PubMed=9054939;  
 RA Fleury C., Neverova M., Collins S., Raimbault S., Champigny O.,  
 RA Levi-Meyrueis C., Bouillaud F., Seidlin M.F., Suric R.S.,  
 RA Ricquier D., Warden C.H.;  
 RT "uncoupling protein-2: a novel gene linked to obesity and  
 RT hyperinsulinemia.";  
 RL Nat. Genet. 15:269-272(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANT VAL-55.  
 RC TISSUE=Spleen;  
 RA MEDLINE=97278985; PubMed=9133562;  
 RA Gimeno R.E., Dembeki M., Weng X., Deng N., Shyjan A.W.,  
 RA Glamo C.J., Irls F., Ellis S.J., Woolf B.A., Tartaglia L.A.;  
 RT "Cloning and characterization of an uncoupling protein homolog: a  
 RT potential molecular mediator of human thermogenesis.";  
 RL Diabetes 46:900-906(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANT VAL-55.

RA Klannemark M., Orho M., Groop L.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98227655; PubMed=9568704;  
 RA Argyropoulos G., Brown A.M., Peterson R., Likes C.E., Watson D.K.,  
 RA Garay W.T.;  
 RT "Structure and organization of the human uncoupling protein 2 gene and  
 RT identification of a common biallelic variant in Caucasian and African-  
 RT American subjects.";  
 RL Diabetes 47:685-687(1998).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=99185293; PubMed=10082652;  
 RA Requeux C., Cassard-Douclier A.M., Raimbault S., Miroux B.,  
 RA Fleury C., Gelly C., Bouillaud F., Ricquier D.;  
 RT "Functional organization of the human uncoupling protein-2 gene, and  
 RT juxtaposition to the uncoupling protein-3 gene.";  
 RL Biochem. Biophys. Res. Commun. 255:40-46(1999).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maiz M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create  
 CC proton leaks across the inner mitochondrial membrane, thus  
 CC uncoupling oxidative phosphorylation from ATP synthesis. As a  
 CC result, energy is dissipated in the form of heat.  
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult human tissues,  
 CC including tissues rich in macrophages. Most expressed in white  
 CC adipose tissue and skeletal muscle.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- SIMILARITY: Contains 3 solar repeats.  
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 CC -----  
 DR EMBL; U62819; AAC51336.1; -  
 DR EMBL; U76367; AAB48411.1; -  
 DR EMBL; U94592; AAB53091.1; -  
 DR EMBL; AJ223477; CA11402.1; -  
 DR EMBL; AJ223478; CA11402.1; -  
 DR EMBL; AJ223479; CA11402.1; JOINED.  
 DR EMBL; AF019409; AAC39690.1; -  
 DR EMBL; AF096289; AAD21151.1; -

DR EMBL: BC011737; AAH1737.1; -.  
 DR GenBank: HGNC:12518; UCP2.  
 DR MIM: 601693; .  
 DR GO: GO:0015302; F: uncoupling protein activity; TAS.  
 DR GO: GO:0015992; P: proton transport; TAS.  
 DR InterPro: IPR002030; Mlt uncoupling.  
 DR InterPro: IPR001993; Mlt carrier.  
 DR Pfam: PF00153; mltcarr; 3.  
 DR PRINTS: PR00784; MTUNCPLING.  
 DR PROSITE: PS50920; SOLCAR; 3.  
 DR Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;  
 KM Polymorphism.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 78 100 2 (POTENTIAL).  
 FT TRANSMEM 120 136 3 (POTENTIAL).  
 FT TRANSMEM 181 197 4 (POTENTIAL).  
 FT TRANSMEM 215 234 5 (POTENTIAL).  
 FT TRANSMEM 269 291 6 (POTENTIAL).  
 FT REPEAT 11 106 SOLCAR 1.  
 FT REPEAT 114 203 SOLCAR 2.  
 FT REPEAT 212 297 SOLCAR 3.  
 FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY  
 FT SIMILARITY).  
 FT VARIANT 55 55 A -> V (in dbSNP:660339).  
 FT CONFLICT 219 219 /FTID=VAR 016129.  
 FT SEQUENCE 309 AA; 33229 MM; 28174139162183D9 CRC64;  
 SQ  
 Query Match 71.0%; Score 1149.5; DB 1; Length 309;  
 Best Local Similarity 72.2%; Pred. No. 7.6e-98;  
 Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MWGLRSDVPPPTMAVKFLGAGTAACTADITPEPLDTAKRLOIOGENQA-VQTARLVQYR 59  
 DB 1 MWGFRATDVPPTATYKFLGAGTAACTADITPEPLDTAKRLOIOGSGQPVAAASQYR 60  
 QY 60 GVLGTTILMTWRTGSPSPYNGIYAGIQRQMSFASIRIGLYDSVKQYTPKGDNSLTLR 119  
 DB 61 GVMGTTILMTWRTGSPSPYNGIYAGIQRQMSFASIRIGLYDSVKQYTPKGDNSLTLR 119  
 QY 120 ILAGCTTGAMANTCAQPTDVVVRFOASIHIGPSRSDRYSGTMDAYRTIAREEGVGLM 179  
 DB 120 ILAGSTTGALAAVAQPTDVVVRFOAARAG---SGRRYQSTVDYKTIAREEGFRGLM 176  
 QY 180 KGTLPNIMNNAIYNCAEVVYTDILKEKLDYHLTDNPFCHVSAAGAFCAITVASPYD 239  
 DB 177 KGTSPVARNNAIYNCAELVYTDILKDALIKANIMTDLPCHFTSAAGAFCTTIVASPYD 236  
 QY 240 VKTRRYMNSPPQGYRSPLDCKIMVAQSGPTAFYKGFSPRLSGSNVVMFVYEQQLR 299  
 DB 237 VKTRRYMNSALQGYSSAGHCALTMLOKSGPRAFYKGFSPRLSGSNVVMFVYEQQLR 296  
 QY 300 ALMKVQMLRESPF 312  
 DB 297 ALMAACTSREAPF 309

RESULT 11  
 UCP2 CANFA STANDARD; PRT; 309 AA.  
 AC 09N2T1: 09TTO:  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mitochondrial uncoupling protein 2 (UCP 2).  
 OS UCP2.  
 GN Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ishioh K.;

RT "Cloning of canine UCP families."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 4-197 FROM N.A.  
 RA Thompson G.M., Kelly L.J., Candelore M.R.,  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create  
 CC proton leaks across the inner mitochondrial membrane, thus  
 CC uncoupling oxidative phosphorylation from ATP synthesis. As a  
 CC result, energy is dissipated in the form of heat (By similarity).  
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- SIMILARITY: Contains 3 Solcar repeats.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL: AB020887; BAA30457.1; -.  
 CC DR EMBL: AF201377; AAF08309.1; -.  
 CC DR InterPro: IPR002030; Mlt uncoupling.  
 CC DR InterPro: IPR001993; Mlt carrier.  
 CC DR Pfam: PF00153; mltcarr; 3.  
 CC DR PRINTS: PR00784; MTUNCPLING.  
 CC DR PROSITE: PS50920; SOLCAR; 3.  
 CC DR Mitochondrion: Transmembrane; Repeat.  
 FT TRANSMEM 11 32 1 (POTENTIAL).  
 FT TRANSMEM 78 100 2 (POTENTIAL).  
 FT TRANSMEM 120 136 3 (POTENTIAL).  
 FT TRANSMEM 181 197 4 (POTENTIAL).  
 FT TRANSMEM 215 234 5 (POTENTIAL).  
 FT TRANSMEM 269 291 6 (POTENTIAL).  
 FT REPEAT 11 106 SOLCAR 1.  
 FT REPEAT 114 203 SOLCAR 2.  
 FT REPEAT 212 297 SOLCAR 3.  
 FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY  
 FT SIMILARITY).  
 FT CONFLICT 64 64 C -> G (IN REF. 2).  
 FT SEQUENCE 309 AA; 33270 MM; D9860F0EA8B70BF CRC64;  
 SQ  
 Query Match 70.7%; Score 1145.5; DB 1; Length 309;  
 Best Local Similarity 72.5%; Pred. No. 1.8e-97;  
 Matches 227; Conservative 29; Mismatches 52; Indels 5; Gaps 3;

QY 1 MWGLRSDVPPPTMAVKFLGAGTAACTADITPEPLDTAKRLOIOGENQA-VQTARLVQYR 59  
 DB 1 MWGFRATDVPPTATYKFLGAGTAACTADITPEPLDTAKRLOIOGSGQPVAAASQYR 60  
 QY 60 GVLGTTILMTWRTGSPSPYNGIYAGIQRQMSFASIRIGLYDSVKQYTPKGDNSLTLR 119  
 DB 61 GVMGTTILMTWRTGSPSPYNGIYAGIQRQMSFASIRIGLYDSVKQYTPKGDNSLTLR 119  
 QY 120 ILAGCTTGAMANTCAQPTDVVVRFOASIHIGPSRSDRYSGTMDAYRTIAREEGVGLM 179  
 DB 120 ILAGSTTGALAAVAQPTDVVVRFOAARAG---SGRRYQSTVDYKTIAREEGFRGLM 176  
 QY 180 KGTLPNIMNNAIYNCAEVVYTDILKEKLDYHLTDNPFCHVSAAGAFCAITVASPYD 239  
 DB 177 KGTSPVARNNAIYNCAELVYTDILKDALIKANIMTDLPCHFTSAAGAFCTTIVASPYD 236  
 QY 240 VKTRRYMNSPPQGYRSPLDCKIMVAQSGPTAFYKGFSPRLSGSNVVMFVYEQQLR 299  
 DB 237 VKTRRYMNSALQGYSSAGHCALTMLOKSGPRAFYKGFSPRLSGSNVVMFVYEQQLR 296  
 QY 300 ALMKVQMLRESPF 312  
 DB 297 ALMAACTSREAPF 309

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RESULT 12
UCP2_CYPCA STANDARD; PRT: 310 AA.
ID UCP2_CYPCA
AC 09W725;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 2 (UCP 2).
GN UCP2.
OS Cypinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Stuart J.A., Harper J.A., Brindle K.M., Brand M.D.;
RT "Uncoupling protein 1 homologues and thermogenesis? UCP2 from cold-
RT blooded vertebrates."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
CC proton leaks across the inner mitochondrial membrane, thus
CC uncoupling oxidative phosphorylation from ATP synthesis. As a
CC result, energy is dissipated in the form of heat (By similarity).
CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
-----
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-----
DR EMBL: AJ243486; CAB46248.1; -.
DR InterPro: IPR002030; Mitc_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_cartr; 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 79 101
FT TRANSMEM 121 137
FT TRANSMEM 182 198
FT TRANSMEM 216 235
FT TRANSMEM 270 292
FT REPEAT 11 107
FT REPEAT 115 204
FT REPEAT 213 298
FT REPEAT 277 299
FT DOMAIN
SQ SEQUENCE 310 AA; 33532 MW; AD0B4D73C73704E CRC64;

Query Match 69.2%; Score 1121; DB 1; Length 310;
Best Local Similarity 72.4%; Pred. No. 3.1e-95;
Matches 220; Conservative 31; Mismatches 47; Indels 6; Gaps 4;

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DB 120 RLMGCTTGAMVAVLAQPTDVVVRFOASIHGSPSMDKRYSGTMDAYRTIABEGVRGL 178
QY 179 WKGTLPNIRNAIYNCAEVVYDILKEKLLDYHLITDNFPCHFVAFAGPATVVASPV 238
DB 177 WKGTSPNITRNAIYNCTELVYDILKDALILKSLMTDLPCHFTSAFAGFCTVYIASPV 236
QY 239 DVVKTIRVNSPPGOYFSPLDCKIKVNAQEGPTAFYKGFPTSPFLRGSNNVVFVYEQLK 298
DB 237 DVVKTIRVNSAPGOYCSALNCVAMLTLYGPKAFYKGFPTSPFLRGSNNVVFVYEQLK 296
QY 299 PALM 302
DB 297 RALM 300

RESULT 13
UCP2_BRARE STANDARD; PRT: 310 AA.
ID UCP2_BRARE
AC 09W720;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 2 (UCP 2).
GN UCP2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Stuart J.A., Harper J.A., Brindle K.M., Brand M.D.;
RT "Uncoupling protein 1 homologues and thermogenesis? UCPS from cold-
RT blooded vertebrates."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
CC proton leaks across the inner mitochondrial membrane, thus
CC uncoupling oxidative phosphorylation from ATP synthesis. As a
CC result, energy is dissipated in the form of heat (By similarity).
CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
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CC or send an email to license@isb-sib.ch).
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DR EMBL: AJ243250; CAB46268.1; -.
DR ZFIN: ZDB-GENE-990708-8; ucp2.
DR InterPro: IPR002030; Mitc_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_cartr; 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 79 101
FT TRANSMEM 121 137
FT TRANSMEM 182 198
FT TRANSMEM 216 235
FT TRANSMEM 270 292
FT REPEAT 11 107
FT REPEAT 115 204
FT REPEAT 213 298
FT REPEAT 277 299
FT DOMAIN
SQ SEQUENCE 310 AA; 33532 MW; AD0B4D73C73704E CRC64;

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